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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC
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Related Applications

The present application claims priority to prior filed U.S. Provisional Patent
5 Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent
Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent
Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional
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10 German Patent Application No. 19941394.0, filed August 31, 1999, German Patent Application No. 19941396.7, filed August 31, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German
15 Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942124.2, filed September 3, 1999, and German Patent Application No. 19942129.3, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly
20 incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and
25 pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce
30 and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have

been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

5 Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related
10 bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the
15 degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the
20 invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the
25 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
30 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

diphtheriae (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

- 5 Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, vitamins, cofactors, nutraceuticals,
10 nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and
15 Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an
20 indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway
25 protein may result in an increase in the yield or efficiency of production of lysine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a
30 pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, a vitamin, or a nucleotide may increase the overall

ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention may be utilized to

5 directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a

10 biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of

15 the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily

20 intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino

25 acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes

30 more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), which are capable of, for example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a

sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to catalyze a reaction in a metabolic pathway for an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein
5 can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MP sequence as a
10 transgene. In another embodiment, an endogenous MP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MP gene. In another embodiment, an endogenous or introduced MP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still
15 another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being
20 particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of
25 one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 1156) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MP protein or a
30 portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a

nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression.

Examples of agents which stimulate MP protein activity or MP nucleic acid expression include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules, and antisense MP nucleic acid molecules.

5 Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the
10 introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

15

Detailed Description of the Invention

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and
20 trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase of
25 yield or efficiency of production of the desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). Aspects of the invention are further explicated below.

30

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include

5 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty

10 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids,

15 Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in

20 Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are

25 essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

30 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-

step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

30 B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although

they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic

acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and

biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

5 *C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
10 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or
15 their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

20 Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the
25 development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,
30 folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and

Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

- 5 The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology,
- 10 Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or
- 15 adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP).
- 20 The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

25 D. *Trehalose Metabolism and Uses*

- Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.
- 30 Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from

many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

5 The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules, which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic
10 pathways. In a preferred embodiment, the activity of the MP molecules of the present invention in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the
15 *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

 The language, "MP protein" or "MP polypeptide" includes proteins which play
20 a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MP gene" or "MP nucleic acid sequence" include nucleic acid sequences encoding an MP protein, which consist of a
25 coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of
30 production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes

the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and

degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway.

Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C. glutamicum* MP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin,

cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

5

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

30 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the

sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, 5 *T. Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this 10 sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate 15 extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the 20 nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding 25 to an MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the 30 *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated

sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02229 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include *C. glutamicum* those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs

of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MP

5 homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one

10 of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone MP homologues. Probes based on the MP nucleotide sequences can be used to detect transcripts or

15 genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding

20 nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-

25 numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or

30 equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the

protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00219 (SEQ ID NO:345). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences set forth in the
5 Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms
10 "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein, preferably a *C. glutamicum* MP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid
15 polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard
20 hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
25 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
30 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

- 10 In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MP proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity.
- 15
- 20 Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP activity.

- Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential for MP activity. Such MP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic
- 25
- 30

acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic

acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA02229) comprises nucleotides 1 to 825). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense

nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For

5 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an

10 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified

15 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

20 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-

25 methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from

30 the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by
5 conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or
10 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

15 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a
20 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they
25 have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO: 1
30 (RXA02229). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.*

U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

5 Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and
10 Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As
15 used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
20 autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
25 which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
30 such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is
- 5 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory
- 10 sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).
- 15 Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *arny*, *SPO2*, λ -*P_R*- or λ *P_L*, which are used preferably in bacteria.
- 20 Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such
- 25 factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins, fusion proteins, etc.).
- 30 The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus

expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- 5 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 10 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 15 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 20 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the
- 25 recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum*
- 30 (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) 5 *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge 10 University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* 15 (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include 20 those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: 25 New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the 30 expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both

prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

5 In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* 10 (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), 15 pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) 20 *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an 25 RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA.

30 The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell

type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be
5 introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which
10 contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous
15 recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the
20 endogenous MP protein). In the homologous recombination vector, the altered portion of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous
25 recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the
30 endogenous MP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*,
5 by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or
10 inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present
15 invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention further provides methods for producing MP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of
20 invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

25

C. Isolated MP Proteins

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA
30 techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP protein in which the protein is separated from cellular components of the cells in which

it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still
5 more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The
10 language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical
15 precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism
20 from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide,
25 nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic
30 reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of

the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%,

78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP activities described herein. Ranges and identity values
5 intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire
10 amino acid sequence of the invention.

Biologically active portions of an MP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MP protein, e.g., an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino
15 acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in
20 which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For
25 example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein,
30 polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (e.g., endothelial

cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively
5 linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the
10 fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins
15 can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by
20 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid
25 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric
30 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue" refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

In an alternative embodiment, homologues of the MP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C.*

glutamicum sequences of interest; evolutionary studies; determination of MP protein regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

- 5 The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the
- 10 extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*.
- 15 *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
- 20 inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at
- 25 least 5,000 deaths since 1990.

 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in

30 the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum*

are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism
5 expressing one or more MP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a
10 nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the
15 gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to
20 decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is
25 capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned
30 compounds, the modulation of activity of one of the proteins of the invention may still impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely

interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By

these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any
5 natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not
10 be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Included Genes

Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXA02229	GR00653	2793	3617	DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

Trehalose

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
17	18	RXN00351	VV0135	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00066	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00241	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00243	1005	4	trehalose synthase (EC 2.4.1.-)

Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18)
33	34	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
39	40	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VV0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA00972	GR00274	3	1379	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Glutamate and glutamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
71	72	RXN00367	VV0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VV0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VV0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VV0196	14607	15233	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
95	96	RXA00323	GR00057	3855	5192	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
97	98	RXA00335	GR00057	19180	17750	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
99	100	RXA00324	GR00057	5262	8396	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
101	102	RXN03176	VV0332	2	862	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
103	104	F RXA02879	GR10017	2	862	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
107	108	RXA00727	GR00193	614	1525	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)
Alanine and Aspartate and Asparagine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	VV0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	VV0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
125	126	RXA02432	GR00708	2669	1695	ASPARTATE AMONIA-LYASE (EC 4.3.1.1)
127	128	RXN03003	VV0138	680	6	L-ASPARAGINASE (EC 3.5.1.1)
129	130	RXN00508	VV0086	4701	5783	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
131	132	RXN00636	VV0135	20972	19944	ALANINE RACEMASE (EC 5.1.1.1)
						ALANINE RACEMASE, BIOSYNTHETIC (EC 5.1.1.1)

beta-Alanine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RXS00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RXS02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

Glycine and serine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	VV0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00766	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	VV0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RXS01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RXS03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Table 1 (continued)

Threonine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
169	170	RXN00969	VW0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE METABOLISM

Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RX503158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RX503159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
201	202	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
203	204	RXN00402	VW0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VW0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VW0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
219	220	RXN00132	VW0124	3612	5045	ADENOSYLMHOMOCYSTEINASE (EC 3.3.1.1)
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLMHOMOCYSTEINASE (EC 3.3.1.1)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	F RXA01371	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
227	228	F RXA02085	GR00629	3496	5295	METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
231	232	RXN02648				METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
235	236	F RXA02658	GR00752	14764	15447	METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
239	240	RXC00128				METHYLTRANSFERASE (EC 2.1.1.14)
						PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES
						AND PANTOTHENATE
						EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND
						ADENOSYLHOMOCYSTEINE

S-adenosyl methionine (SAM) Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

Cysteine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Table 1 (continued)

Valine, leucine and isoleucine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
257	258	RXA02646	GR00751	3856	2588	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXN01127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXN00536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
281	282	F RXA01929	GR00555	2766	1960	/ DECARBOXYLASE (EC 4.1.1.44)
283	284	RXN01420	VV0122	15584	14643	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
285	286	RXS01145				4'-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.3.1.1)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

Arginine and proline metabolism

Enzymes of proline biosynthesis:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Table 1 (continued)

Enzymes of proline degradation:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
307	308	RXN00023	VV0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

Synthesis of 3-Hydroxy-proline:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXA01491	GR00423	5337	4687	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS

Enzymes of ornithine, arginine and spermidine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VV0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
333	334	RXA02158	GR00640	5268	6224	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
335	336	RXA02160	GR00640	6914	8116	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
337	338	RXN02162	VV0122	6683	5253	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
339	340	F RXA02161	GR00640	8180	8962	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
345	346	RXA00219	GR00032	19289	20230	SERMIDINE SYNTHASE (EC 2.5.1.16)
347	348	RXA01508	GR00424	12652	14190	SERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	PUTRESCINE OXIDASE (EC 1.4.3.10)
351	352	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
353	354	RXN02154	VV0122	13327	13037	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
355	356	RXS00147				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
357	358	RXS00905				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Histidine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01097	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
385	386	RXN01657	VV0010	39950	39351	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
389	390	RXA01098	GR00306	5499	4726	HISF PROTEIN
391	392	RXN01104	VV0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXN00446	VV0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXA01105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

Metabolism of aromatic amino acids

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIMKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
415	416	RXN00954	VV0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VV0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
423	424	RXA02687	GR00754	11306	12250	CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VW0134	11507	12736	CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991	CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128	ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
437	438	RXA02093	GR00629	12444	13247	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
439	440	RXA02791	GR00777	6968	7795	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
441	442	RXA01699	GR00477	984	1553	SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VW0247	1140	4	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
449	450	RXA00064	GR00010	2499	3776	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
451	452	RXN00448	VW0112	33959	32940	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	3	668	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	F RXA00452	GR00110	854	1099	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VW0208	3410	3778	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VW0086	25447	25887	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VW0182	7497	6886	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VW0182	10347	11099	3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
479	480	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
481	482	RXS00446				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
493	494	RXS02315				2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGlutarate decarboxylase (EC 4.1.1.71)
495	496	RXS02550				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319				NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026				3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
505	506	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

Aminobutyrate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXN02970	VV0021	4714	6081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Vitamins, vitamin-like substances (cofactors), nutraceuticals

Thiamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
549	550	RXS01807				PYRIDOXINE KINASE (EC 2.7.1.35)
551	552	RXC01021				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN

Table 1 (continued)

Riboflavin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase [EC 1.1.1.193]
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC 3.5.4.-]
557	558	RXA02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC 3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmrl synthase, lumazine synthase, riboflavin synthase beta chain) [EC 2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE
573	574	RXA01489	GR00423	3410	2388	PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380	GR00691	709	56	Predicted nucleotidyltransferases
591	592	RXC02921				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

Vitamin B6 metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

Table 1 (continued)
Nicotinate (nicotinic acid), nicotinamide, NAD and NADP

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

NAD Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

Pantothenate and Coenzyme A (CoA) biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDRO-PANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

Biotin metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VW0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VW0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

Lipoic Acid

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
661	662	RXA01747	GR00495	2506	3549	LIPIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LIPIC ACID SYNTHETASE
665	666	RXA02106	GR00632	472	1527	LIPIC ACID SYNTHETASE
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LIPIC ACID SYNTHETASE
671	672	RXS01261				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)

Folate biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VW0296	503	1003	5-FORMYLTHETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTHETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VW0082	8868	9788	FORMYLTHETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTHETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE DEHYDROGENASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	VV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

Molybdopterin Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
733	734	RXN02802	VV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	VV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	VV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
783	784	RXA02318	GR00665	9684	9962	(D90909) pterin-4a-carbinolamine dehydratase [Synchocystis sp.]
785	786	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304	VV0148	4449	4934	MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556				FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-) / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)

Vitamin B₁₂, porphyrins and heme metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
813	814	RXN01162	VV0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
815	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	818	RXA01692	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
819	820	RXN00371	VV0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VV0223	4206	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
829	830	F RXA00383	GR00082	3876	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
832	832	RXA01253	GR00365	2536	1787	COBYRIC ACID SYNTHASE
833	834	RXA02134	GR00639	1721	801	COBALAMIN (5'-PHOSPHATE) SYNTHASE
835	836	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
837	838	RXA02136	GR00639	3362	2841	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
839	840	RXN03114	VV0088	1	552	COBG PROTEIN (EC 1.-.-)
841	842	RXN01810	VV0082	1739	663	HEMN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
843	844	RXS03205				HEMK PROTEIN
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

Vitamin C precursors

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
849	850	RXN00420	VV0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VV0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
861	862	RXS00389				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
863	864	RXS00419				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
865	866	RXC00416				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				

Vitamin K2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
871	872	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYL BENZOIC ACID-COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYL BENZOIC ACID-COA LIGASE (EC 6.2.1.26)

Ubiquinone biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLUBIQUINONE-9-3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLUBIQUINONE-9-3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLUBIQUINONE-9-3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

Purines and Pyrimidines and other Nucleotides

Regulation of purine and pyrimidine biosynthesis pathways

Purine metabolism

Purine Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE, PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE, GARS (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) / PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (EC 2.1.2.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00620	GR00163	3049	3939	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLYL KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLYL KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

Table 1 (continued)

GMP/AMP degrading activities

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
967	968	RXA00489	GR00121	654	1775	GMP REDUCTASE (EC 1.6.6.8)
969	970	RXN02281	VW0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
971	972	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

Pyrimidin metabolism

Pyrimidine biosynthesis de novo:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
973	974	RXA00147	GR00022	9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
975	976	RXA00145	GR00022	7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
977	978	RXA00146	GR00022	8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
979	980	RXA02208	GR00647	2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
981	982	RXA01660	GR00462	591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
983	984	RXA02235	GR00654	3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
985	986	RXN01892	VW0150	3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
987	988	F RXA01892	GR00542	47	775	URIDYLATE KINASE (EC 2.7.4.-)
989	990	RXA00105	GR00014	16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
991	992	RXA00131	GR00020	7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
993	994	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
995	996	RXA00718	GR00188	4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
997	998	RXA01599	GR00447	8780	10441	CTP SYNTHASE (EC 6.3.4.2)
999	1000	RXN02234	VW0134	24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1001	1002	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1003	1004	RXN00450	VW0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1005	1006	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1007	1008	RXN02272	VW0020	15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
1009	1010	F RXA02272	GR00655	6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1011	1012	RXN03004	VW0237	1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1013	1014	RXN03137	VW0129	9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1015	1016	RXN03171	VW0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1017	1018	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

Table 1 (continued)

Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:
Purines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VW0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VW0143	5761	6768	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	F RXA01027	GR00294	2580	2347	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5853	5126	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00537	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VW0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VW0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VW0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)

Pyrimidine and purine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1057	1058	RXN01940	VW0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VW0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VW0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00550	1321	908	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (EC 1.17.4.1)
1075	1076	RXA01080	GR00301	1240	797	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1077	1078	RXA00867	GR00237	1	627	NRDI PROTEIN
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1083	1084	RXA01678	GR00467	7162	7689	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VW0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

Pyrimidines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1105	1106	RXN03171	VW0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VW0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VW0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VW0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1133	1134	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND ADENOSYLMOCYSTEINE
1135	1136	RXC01709				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM

Table 1 (continued)

Sugars

Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				Hypothetical Trehalose Transport Protein
1153	1154	RXS03183				TREHALOSE/MALTOSE BINDING PROTEIN
1155	1156	RXC00874				TRANSMEBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?, high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A I 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A I 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A I 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A I 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A I 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A I 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A I 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A I 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A I 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A I 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A I 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A I 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosoli, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranyl phosphate transferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; cgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cgIIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxido-reductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diptheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap; pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the <i>espI</i> gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the <i>cspB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

	leuA	Isopropylmalate synthase	
X70959			Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,'" <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Siewe, R. M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Vrlić, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum A TCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; fsq/divD; ftsZ	UDP-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of ϕ phi304L: An integrase module among corynebacteriophages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
* A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NGTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rx000044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created) 07-OCT-1996
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	17-DEC-1993
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	28-Jul-99
rx000064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	31,111	2-Aug-99
rx000072		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx00105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx00106	579	GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCICGAP_Pf6 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ; mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rx00115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK 472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

Table 4 (continued)

rx00116	1284	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus SstI (sstI), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannosyltransferase (lpsD), putative mannosyltransferase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds. Sequence 6 from patent US 5500353.	Unknown.	36,235	19-OCT-1999
		GB_PAT:118647	3300	118647			36,821	07-OCT-1996
		GB_GSS13:AQ44619	751	AQ446197	nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0062D16r, genomic survey sequence.	Oryza sativa	38,124	8-Apr-99
rx00131	732	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rx00132	1557	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TVU40872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPCI-98 36 D.15 map 13C-13E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rx00145	1059	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L.leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rx00146	1464	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rx00147	1302	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rx00156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10.	Streptomyces coelicolor	52,666	10-Feb-99

Table 4 (continued)

GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasins 1 (inv1), invasins 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	54,191	26-MAR-1998
GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	46,667	6-Feb-99
GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	37,451	21-Aug-99
GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	37,451	21-Aug-99
GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3L/62B1 clone RPC198-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	38,627	16-OCT-1999
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	92,113	13-MAR-1999
GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	93,702	13-MAR-1999
GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	34,221	31-Jan-99
GB_HTG2:HSDJ850E	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	37,965	03-DEC-1999
GB_HTG2:HSDJ850E	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	37,965	03-DEC-1999
GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	38,796	11-Nov-99
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	38,227	22-Nov-98
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	38,227	22-Nov-98
GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	38,227	22-Nov-98
GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	48,826	2-Aug-96
GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	40,135	22-MAR-1999
GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L/70C1 clone RPC198-9B18, *** SEQUENCING IN PROGRESS ***; 64 unordered pieces.	39,527	16-OCT-1999
GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	98,237	18-MAY-1999
GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	36,616	18-Apr-98
GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	37,095	26-Feb-99
GB_BA1:CGLYSI	4232	X60312	C.glutamicum lysI gene for L-lysine permease.	100,000	30-Jan-92

Table 4 (continued)

	GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.				Plasmodium falciparum	34,947	11-Aug-99
	GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.				Plasmodium falciparum	34,947	11-Aug-99
rx00262	1197	GB_IN2:EHU89655 3219	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.				Entamoeba histolytica	36,496	23-MAY-1997
		GB_IN2:EHU89655 3219	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.				Entamoeba histolytica	37,544	23-MAY-1997
rx00266	531	GB_RO:AF016190 2939	Mus musculus connexin-36 (Cx36) gene, complete cds.				Mus musculus	41,856	9-Feb-99
		EM_PAT:E09719 3505	DNA encoding precursor protein of alkaline cellulase.				Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
rx00278	1155	GB_PAT:E02133 3494	gDNA encoding alkaline cellulase.				Bacillus sp.	34,741	29-Sep-97
		GB_IN1:CELK05F6 36912	Caenorhabditis elegans cosmid K05F6.				Caenorhabditis elegans	36,943	6-Jan-98
		GB_BA1:CGU43535 2531	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.				Corynebacterium glutamicum	36,658	9-Apr-97
rx00295	1125	GB_RO:RNU30789 3510	Rattus norvegicus clone N27 mRNA.				Rattus norvegicus	38,190	20-Aug-96
		GB_BA2:CGU31281 1614	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.				Corynebacterium glutamicum	99,111	21-Nov-96
		GB_BA1:BRLBIOBA 1647	Brevibacterium flavum gene for biotin synthetase, complete cds.				Corynebacterium glutamicum	98,489	3-Feb-99
		GB_PAT:E03937 1005	DNA sequence encoding Brevibacterium flavum biotin-synthase.				Corynebacterium glutamicum	98,207	29-Sep-97
rx00323	1461	GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.				Mycobacterium tuberculosis	35,615	24-Jun-99
		GB_BA1:MSGGB32CS 36404	Mycobacterium leprae cosmid B32 DNA sequence.				Mycobacterium leprae	60,917	15-Jun-96
rx00324	3258	GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.				Mycobacterium tuberculosis	44,606	24-Jun-99
		GB_BA1:MSGGB32CS 36404	Mycobacterium leprae cosmid B32 DNA sequence.				Mycobacterium leprae	52,516	15-Jun-96
		GB_BA1:MTCY427 38110	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.				Mycobacterium tuberculosis	38,079	24-Jun-99
rx00330	1566	GB_OM:BOVELA 3242	Bovine elastin a mRNA, complete cds.				Bos taurus	39,351	27-Apr-93
		GB_BA1:CGTHRC 3120	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).				Corynebacterium glutamicum	99,808	17-Jun-97
		GB_PAT:109078 3146	Sequence 4 from Patent WO 8809819.				Unknown.	99,617	02-DEC-1994
		GB_BA1:BLTHRESY 1892	Brevibacterium lactofermentum; ATCC 13869; DNA (genomic);				Corynebacterium glutamicum	99,170	20-Sep-95
rx00335	1554	GB_BA1:CGGLNA 3686	Corynebacterium glutamicum glnA gene.				Corynebacterium glutamicum	100,000	28-Aug-97

Table 4 (continued)

	GB_BA2:AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
	GB_BA1:MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
rx00347	891	GB_EST27:AI455217	624	AI455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828.3prime, mRNA sequence.	Drosophila melanogaster	34,510
		GB_BA2:SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site 1 for vector use.	Synechococcus PCC7942	09-MAR-1999
		GB_EST21:AA911262	581	AA911262	oe75a02.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418.3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN); mRNA sequence.	Homo sapiens	21-Apr-98
rx00351	1578	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	09-MAR-1995
		GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	17-Jul-98
		GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA, GH08860 (BcDNA, GH08860) mRNA, complete cds.	Drosophila melanogaster	14-Jun-99
rx00365	727	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	16-Aug-99
rx00366	480	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	16-Aug-99
rx00367	4653	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	16-Aug-99
rx00371	1917	GB_VI:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2, and 3 DNA, complete cds.	Sugarcane bacilliform virus	12-Jun-93
		GB_EST37:AI967505	380	AI967505	Ljirpest03-215-c10 Ljirnp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	24-Aug-99
		GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	22-Jan-98

Table 4 (continued)

rx00377	1245	GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
rx00382	1425	GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
		GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_Q_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38:AW01705	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
rx00402	623	GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
		GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI11288	750	AI11288	SWOVAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02A05 5' mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

Table 4 (continued)

rx00405	613	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	57,259	23-Jun-99
		GB_PR4:AC005145	143678	AC005145	Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	40,169	23-Jun-99
rx00420	1587	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	62,031	17-Jun-98
		GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	61,902	10-DEC-1996
		GB_BA1:MSGB971C	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium leprae	39,651	15-Jun-96
rx00435	1296	GB_BA1:AFACBBTZ	2760	M68904	Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds.	Ralstonia eutropha	38,677	27-Jul-94
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rx00437	579	GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	31,738	18-Nov-98
		GB_BA1:SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11.	Streptomyces coelicolor	43,262	5-Aug-98
		GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	37,647	18-Nov-98
rx00439	591	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	37,088	23-Jun-99
		GB_PL2:AF167358	1022	AF167358	Rumex acetosa expansin (EXP3) gene, partial cds.	Rumex acetosa	46,538	17-Aug-99
		GB_HTG3:AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPC1-11_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.	Homo sapiens	43,276	3-Aug-99
rx00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	42,931	4-Jun-98
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	36,702	4-Jun-98
rx00441	1287	GB_PR2:HS173D1	117338	AL031984	Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33 Contains ESTs, STSs and GSSs, complete sequence.	Homo sapiens	38,027	23-Nov-99
		GB_HTG2:HSDJ719K	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
		GB_HTG2:HSDJ719K	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
rx00446	987	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	56,410	26-Nov-98
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999

Table 4 (continued)

rx000448	1143	GB_PR3:AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	35,682	9-Jun-98
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***; 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
rx000450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPC1-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPC1-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:AI818057	412	AI818057	wk14a08.x1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rx000461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC8E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
rx000465		GB_GSS15:AQ64032	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rx000487	1692	GB_BA1:BAGUAA	3866	Y10499	B.ammoniaenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
rx000488	1641	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
rx000489	1245	GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rx000533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97

Table 4 (continued)

	GB_BA1:CGCYSCAS	1591	X82928	C. glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
	GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
rx00534	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
	GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavescens	98,701	11-Jun-93
	GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
rx00536	GB_BA1:CGLEUA	3492	X70959	C. glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
	GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97
rx00537	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
	GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
	GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rx00541	GB_PAT:I92052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
	GB_BA1:MLC85	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rx00558	GB_BA1:BAPURF	1885	X91252	B. ammoniagenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
	GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
	GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
rx00579	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
	EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rx00580	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98

Table 4 (continued)

GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created) 24-Jun-98
GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
GB_EST28:A1534381	581	A1534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: Ani FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome, segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93
GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome, segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995

Table 4 (continued)

rx00632	795	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for dethiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
rx00633	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
rx00688	666	GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rx00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
rx00717	1083	GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	I298268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rx00718	831	GB_BA1:MTCI125	37432	I298268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	I298268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ42075	671	AQ42075	RPCL-11-168G18.TJ RPCL-11 Homo sapiens genomic clone RPCL-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rx00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCL-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCL-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99

Table 4 (continued)

GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	33,888	6-Aug-99
GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS***, 2 unordered pieces.	36,737	25-Feb-99
GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS***, 2 unordered pieces.	36,737	25-Feb-99
GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	36,526	29-MAY-1997
GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	66,193	24-Jun-99
GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	61,443	09-MAR-1995
GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	59,938	21-Sep-99
GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS***, in unordered pieces.	64,896	14-OCT-1998
GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS***, in unordered pieces.	64,896	14-OCT-1998
GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	57,970	3-Nov-99
GB_BA1:MTCV98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	54,410	17-Jun-98
GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	51,729	26-Apr-93
GB_BA2:AF001780	6701	AF001780	Cyanothece PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	36,309	08-MAR-1999
GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	44,308	11-MAR-1994
GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	35,571	28-DEC-1998
GB_EST37:AI998439	455	AI998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	36,044	8-Sep-99
GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,539	16-Aug-93
GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	99,539	28-Jul-99
GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	99,539	28-Jul-99
GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,885	16-Aug-93
GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	100,000	1-Apr-93

Table 4 (continued)

rx000865	1026	GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
		GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	Corynebacterium glutamicum	99,805	28-Jul-99
rx000867	650	GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
		GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds.	Streptomyces antibioticus	59,706	25-OCT-1996
rx000873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,617	29-MAR-1999
rx000884	1263	GB_BA1:D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds.	Pimelobacter sp.	60,594	5-Feb-99
		GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,785	17-Jun-98
		GB_BA1:MSGY222	41156	AD000010	Mycobacterium tuberculosis sequence from clone y222.	Mycobacterium tuberculosis	38,006	03-DEC-1996
		GB_GSS15:AQ65460	468	AQ654600	Sheared DNA-1O14.TF Sheared DNA Trypanosoma brucei genomic clone 0	Trypanosoma brucei	33,974	22-Jun-99
rx000891	1102	GB_BA1:MTCI418B	11700	Z96071	Sheared DNA-1O14, genomic survey sequence.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Mycobacterium tuberculosis H37Rv complete genome; segment 7/162.	Mycobacterium tuberculosis	61,965	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,727	29-MAR-1999
rx000952	963	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	99,688	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,847	10-Feb-99
rx000954	644	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	unidentified	98,428	29-Sep-97
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,758	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	unidentified	98,758	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
rx000955	1545	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97

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								Brevibacterium lactofermentum tryptophan operon.	X04960	7725	GB_BA1:BLTRP				Corynebacterium glutamicum	98,372	10-Feb-99
rx00956	1237							Genomic DNA of trp operon of prepibacterium latophilmentamn.	E01688	7725	GB_PAT:E01688				unidentified	98,242	29-Sep-97
								gDNA encoding tryptophan synthase.	E10963	3118	EM_PAT:E10963			Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created)	
								Brevibacterium lactofermentum tryptophan operon.	X04960	7725	GB_BA1:BLTRP			Corynebacterium glutamicum	99,107	10-Feb-99	
rx00957	1677							DNA sequence of tryptophan operon.	E01375	7726	GB_PAT:E01375			Corynebacterium glutamicum	98,945	29-Sep-97	
								Brevibacterium lactofermentum tryptophan operon.	X04960	7725	GB_BA1:BLTRP			Corynebacterium glutamicum	99,165	10-Feb-99	
								DNA sequence of tryptophan operon.	E01375	7726	GB_PAT:E01375			Corynebacterium glutamicum	98,927	29-Sep-97	
rx00958	747							Genomic DNA of trp operon of prepibacterium latophilmentamn.	E01688	7725	GB_PAT:E01688			unidentified	98,867	29-Sep-97	
								Brevibacterium lactofermentum tryptophan operon.	X04960	7725	GB_BA1:BLTRP			Corynebacterium glutamicum	98,792	10-Feb-99	
								DNA sequence of tryptophan operon.	E01375	7726	GB_PAT:E01375			Corynebacterium glutamicum	98,792	29-Sep-97	
rx00970	1050							Genomic DNA of trp operon of prepibacterium latophilmentamn.	E01688	7725	GB_PAT:E01688			unidentified	98,658	29-Sep-97	
								Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	Y00546	3685	GB_BA1:CGHOMTHR			Corynebacterium glutamicum	99,905	12-Sep-93	
								Sequence 1 from Patent WO 8809819.	I09077	3685	GB_PAT:I09077			Unknown.	99,810	02-DEC-1994	
rx00972	1458							DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK).	E01358	2615	GB_PAT:E01358			Corynebacterium glutamicum	97,524	29-Sep-97	
								gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-IRNA synthase.	E16755	3579	GB_PAT:E16755			Corynebacterium glutamicum	99,931	28-Jul-99	
								Sequence 15 from patent US 5804414.	AR038110	3579	GB_PAT:AR038110			Unknown.	99,931	29-Sep-99	
rx00981	753							DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-IRNA synthase.	E14508	3579	GB_PAT:E14508			Corynebacterium glutamicum	99,931	28-Jul-99	
								Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	AJ245664	512	GB_OV:GGA245664			Gallus gallus	37,538	28-Sep-99	
								Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence.	AC007887	159434	GB_PL2:AC007887			Arabidopsis thaliana	37,600	04-OCT-1999	
rx00989	1644							Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	AL087338	542	GB_GSS1:CNS00RN W			Arabidopsis thaliana	41,264	28-Jun-99	
								Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	AL021246	63033	GB_BA1:MTV008			Mycobacterium tuberculosis	40,773	17-Jun-98	
								S coelicolor valS, fpgs, ndk genes.	Y13070	3619	GB_BA1:SCVALSFP			Streptomyces coelicolor	58,119	03-MAR-1998	
								Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	AL021246	63033	GB_BA1:MTV008			Mycobacterium tuberculosis	38,167	17-Jun-98	

Table 4 (continued)

rx00997	705	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene, complete cds.	Corynebacterium glutamicum	40,841	2-Aug-96
		GB_HTG1:CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,416	26-OCT-1999
		GB_IN1:CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	Caenorhabditis elegans	36,416	2-Sep-99
rx01019	1110	GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_GSS9:AQ171808	512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D	Homo sapiens	34,661	17-OCT-1998
					Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.			
rx01026	1782	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	68,275	15-Jan-99
		GB_BA1:ATLEUCD	2982	X84647	A teichomyceticus leuC and leuD genes.	Actinoplanes teichomyceticus	65,935	04-OCT-1995
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,454	23-Jun-99
rx01027	1131	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	38,636	17-Sep-97
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	51,989	17-Jun-98
		GB_BA1:SPUNG1UT	1172	Z21702	S. pneumoniae ung gene and muX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	Streptococcus pneumoniae	38,088	15-Jun-94
rx01073	954	GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
		GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
		GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
rx01079	2226	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,820	5-Aug-99
		GB_BA1:CANRDFGE	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	75,966	18-Apr-98
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	38,296	23-Jun-99
rx01080	567	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	100,000	5-Aug-99
		GB_BA1:CANRDFGE	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	65,511	18-Apr-98
		GB_BA1:STNRD	4894	X73226	S. typhimurium nrdEF operon.	Salmonella typhimurium	52,477	03-MAR-1997
rx01087	999	GB_IN2:AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	Limnadia lenticularis	43,750	29-MAR-1999
		GB_PR3:HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	Homo sapiens	37,475	23-Nov-99
		GB_IN2:ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	Anathix ralla	37,319	16-Jul-97

Table 4 (continued)

rx01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
rx01100	861	GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
		GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
rx01101	756	GB_HTG1:HSDJ140A	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rx01104	729	GB_BA1:STMHISOPA	3981	M31628	S. coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	26-Apr-93
		GB_BA1:STMHISOPA	3981	M31628	S. coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
rx01106	1449	GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996

Table 4 (continued)

Table 4 (continued)

rx01321	1044	GB_GSS14:AQ51884 441	AQ518843	HS_5106_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2:AC007473 194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 60 unordered pieces.	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG4:AC011696 115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1155) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 108 unordered pieces.	Drosophila melanogaster	38,290	26-OCT-1999
rx01352	706	GB_PL2:ATAC005167 83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825 97380	AC005825	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3:AC011150 127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
rx01360	259	GB_EST32:A1725583 728	A1725583	BNLGH12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U85081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2:HS227P17 82951	Z81007	Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99
		GB_EST34:AV171099 173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 3200002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
rx01361	629	GB_RO:AB008915S1 530	AB008915	Mus musculus mGpi1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22:A1050532 293	A1050532	uc83d10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P. ; mRNA sequence.	Mus musculus	44,097	9-Jul-98
		GB_RO:AB008895 3062	AB008895	Mus musculus mRNA for mGpi1p, complete cds.	Mus musculus	41,316	23-Nov-97
rx01381	944	GB_PL1:AB005237 87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5:AQ766840 491	AQ766840	HS_2026_A2_C09_T7C C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
		GB_BA1:MTV043 68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
rx01393	993	GB_BA1:CGLYSEG 2374	X96471	C. glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7 40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
		GB_PR3:AC004054 112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rx01394	822	GB_BA1:CGLYSEG 2374	X96471	C. glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5:AQ769223 500	AQ769223	HS_3155_B2_G10_T7C C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99

Strain	Genotype	Accession No.	Gene
GB	BA1:CGLYSEG	2374	<i>C. glutamicum lysE</i> and <i>lysG</i> genes.
		X96471	

	GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.			Corynebacterium glutamicum	33,665	24-Feb-97
αa01416	GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.			Streptomyces coelicolor	62,726	10-Aug-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.			Mycobacterium leprae	39,159	22-Aug-97
	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.			Mycobacterium tuberculosis	37,340	17-Jun-98
	GB_BA1:D90827	18886	D90827	E. coli genomic DNA, Kohara clone #336(41.2-41.6 min.).			Escherichia coli	58,517	21-MAR-1997
αa01442	GB_BA1:D90828	14590	D90828	E. coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).			Escherichia coli	56,151	21-MAR-1997
	GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.			Escherichia coli	56,021	12-Nov-98
	GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.			Streptomyces coelicolor	39,037	04-MAY-1999
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.			Mycobacterium tuberculosis	40,130	17-Jun-98
αa01483	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.			Mycobacterium leprae	37,752	27-Aug-99
	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.			Mycobacterium tuberculosis	39,057	17-Jun-98
	GB_BA1:MSGB1229C	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.			Mycobacterium leprae	54,382	15-Jun-96
	GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; IRNA-Asn gene, complete sequence.			Mycobacterium smegmatis	52,941	16-Jan-98
αa01486	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.			Mycobacterium tuberculosis	40,941	17-Jun-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.			Mycobacterium leprae	38,451	22-Aug-97
	GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.			Streptomyces coelicolor	61,194	10-Aug-98
	GB_BA1:CORFADS	1547	D37967	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds.			Corynebacterium ammoniagenes	58,021	8-Feb-99
αa01489	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.			Mycobacterium leprae	38,414	22-Aug-97
	GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.			Streptomyces coelicolor	36,930	9-Jun-99
	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.			Mycobacterium tuberculosis	37,062	17-Jun-98
	GB_EST13:AA356956	255	AA356956	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence.			Homo sapiens	37,647	21-Apr-97
αa01508	GB_OV:OMDNAPROI	7327	X92380	O. mossambicus prolactin I gene.			Tilapia mossambica	38,289	19-OCT-1995
	GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.			Caenorhabditis elegans	37,984	23-Nov-98
	GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.			Caenorhabditis elegans	38,469	23-Nov-98
	GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.			Streptomyces coelicolor	39,021	19-MAY-1999
αa01512	GB_BA1:MAU88875	840	U88875	Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene, complete cds.			Mycobacterium avium	57,521	05-MAR-1997

Table 4 (continued)

GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
GB_PL1:EGGTPCHI	242	Z49757	E. gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1).	Drosophila melanogaster	36,346	13-Aug-99
GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01106 (D1054) RPC1:98 01.1.6 map 55D-55D strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***. 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
GB_PL2:AF038831	647	AF038831	Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	40,566	13-Apr-99
GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from Tq31, complete sequence.	Homo sapiens	36,623	20-Aug-97
GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from Tq31, complete sequence.	Homo sapiens	34,719	20-Aug-97
GB_RO:IMM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
GB_BA1:MTCH125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94

Table 4 (continued)

GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97
GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TF-ujjwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
GB_RO:MMFV1	6480	X97719	M.musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_ma1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence.	Homo sapiens	39,157	29-Nov-95
GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CeiA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
GB_EST22:A1064232	493	A1064232	GH04563 5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neuropeptide F (npf) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
GB_BA2:AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepC) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98

							Mycobacterium leprae cosmid B937 DNA sequence.					
α01699	593	GB_BA1:MSGB937C S	38914	L78820	Myco	B937	DNA sequence.					15-Jun-96
		GB_BA2:AFI24600	4115	AFI24600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.							
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidi) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.							
		GB_EST9:C19712	399	C19712	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.							
α01712	805	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.							
		GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.							
α01719	684	GB_HTG1:HSDJ534K 7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.							
		GB_HTG1:HSDJ534K 7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.							
		GB_EST27:A1447108	431	A1447108	mq91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.							
α01720	1332	GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.							
		GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.							
		GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.							
α01746	876	GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.							
		GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.							
α01747	1167	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.							
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.							
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.							
α01757	924	GB_EST21:AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP:F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E., mRNA sequence.							
		GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNB181 5' end, mRNA sequence.							
		GB_EST20:AA899038	450	AA899038	NCP6G8T7 Peritrichal Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.							

Table 4 (continued)

rx01807	915	GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	40,067	22-Jun-99
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
rx01821	401	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, aml gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	Rattus norvegicus	38,692	15-DEC-1994
rx01835	654	GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY upsilin heavy chain gene, exon 2.	Anas platyrhynchos	36,962	15-Feb-99
		GB_EST30:A1629479	353	A1629479	486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	Zea mays	38,109	26-Apr-99
		GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	37,021	26-MAR-1999
		GB_GSS3:B49052	515	B49052	RPC111-4112.TV RPC111 Homo sapiens genomic clone RPC111-4112, genomic survey sequence.	Homo sapiens	37,021	8-Apr-99
rx01850	1470	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,196	U18997
		GB_BA2:AE000392	10345	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_BA2:U32715	13136	U32715	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,576	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSGB1529C	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	64,260	15-Jun-96
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPC1-98 03.E.19 map 36E.37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGE	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98

Table 4 (continued)

rx01928	960	GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
		GB_BA1:CGPAN	2164	X96580	C. glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
rx01929	936	GB_BA1:CGPAN	2164	X96580	C. glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-96
		GB_BA1:XANHRP86	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
rx01940	1059	GB_IN2:CFU43371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417	18-Jun-96
		GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560	20-Jan-99
rx02022	1230	GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	26-Sep-99
		GB_BA1:CGDAPE	1966	X81379	C. glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAARO	2612	X85965	C. glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	17-Feb-96
rx02024	859	GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome, segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98
		GB_BA1:MSG1912C	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
rx02027		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
rx02031								
rx02072	1464	GB_BA1:CGGDHA	2037	X72855	C. glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	30-Jul-99
		GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99

Table 4 (continued)

rx02085	2358	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
		GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
rx02093	927	GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737	Homo sapiens	34,163	4-Jun-97
		GB_EST17:AA641937	444	AA641937	5', mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
		GB_PR3:AC003074	143029	AC003074	Human PAC clone DJ0596009 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
rx02106	1179	GB_BA1:SC1A6	37620	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
		GB_PR4:AC005553	179651	AC005553	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
		GB_EST3:R49746	397	R49746	yg71g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN); mRNA sequence.	Homo sapiens	41,162	18-MAY-1995
rx02111	1407	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
rx02112	960	GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 Drosophila melanogaster	Drosophila melanogaster	37,909	24-Sep-99
		GB_GSS3:B09839	1191	B09839	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 121 unordered pieces.	Arabidopsis thaliana	37,843	14-MAY-1997
		GB_HTG3:AC010579	157658	AC010579	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,909	24-Sep-99
rx02134	1044	GB_BA1:SCSECYDN	6154	X83011	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 Drosophila melanogaster	Streptomyces coelicolor	36,533	02-MAR-1998
		GB_EST32:AI731596	568	AI731596	09.D.8 map 96F-96F strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 121 unordered pieces.	Gossypium hirsutum	33,451	11-Jun-99
		GB_BA1:SCSECYDN	6154	X83011	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Streptomyces coelicolor	36,756	02-MAR-1998
rx02135	1197	GB_PR3:HS525L6	168111	AL023807	S. coelicolor secY locus DNA.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG Island, complete sequence.	Arabidopsis thaliana	34,325	9-Jun-99
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	33,874	26-Jun-98

Table 4 (continued)

αa02136	645	GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
αa02139	1962	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSG81554C	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1:MSG81551C	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
αa02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
αa02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
αa02155	1287	GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSG81133C	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96
αa02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98

Table 4 (continued)

[illegible]

Table 4 (continued)

rx02176	1251	GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
		GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X66112	C. glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
		GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
rx02189	861	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSGB1970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
rx02193	1701	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
rx02194	966	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
		GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
rx02195	393	GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
		GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
rx02197	551	GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
rx02198	2599	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
rx02208	1025	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
		GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 617.	Aeropyrum pernix	39,442	22-Jun-99

αa02229	948	GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
αa02234	3462	GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-99
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG oritidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993
αa02235	727	GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and oritidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
αa02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J074A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
αa02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
αa02240	1344	EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created 05-MAR-1997)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
		GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds; and Streptomyces spectabilis S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
αa02246	1107	EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created 05-MAR-1997)

Table 4 (continued)

		GB_PAT:E07957	589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
αa02247	756	GB_PAT:I32742	589	I32742	Sequence 1 from patent US 5589355.	Unknown.	52,909	6-Feb-97
		GB_PAT:I32743	2689	I32743	Sequence 2 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel.)
		GB_PAT:I32742	589	I32742	Sequence 1 from patent US 5589355.	Unknown.	57,937	52, Created)
αa02248	1389	GB_PAT:I32742	589	I32742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel.)
		GB_PAT:E07957	589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	52, Created)
		GB_PAT:E07957	589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
αa02250	643	GB_PAT:I32742	589	I32742	Sequence 1 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:I32743	2689	I32743	Sequence 2 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:E07957	589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:I32742	589	I32742	Sequence 1 from patent US 5589355.	Unknown.	56,318	6-Feb-97
αa02262	1269	EM_BA1:AB003693	589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel.)
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	52, Created)
		GB_BA1:CGAMTGEN E	2028	X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_VI:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	Corynebacterium glutamicum	38,651	29-MAY-1996
αa02263	488	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	human herpesvirus 5	100,000	10-Feb-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
		EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel.)
αa02272	1368	GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	52, Created)
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,264	7-Aug-98
		GB_GSS12:AQ41101	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	36,197	20-Feb-99
		0			Homo sapiens genomic clone Plate=2257 Col=3 Row=P _i , genomic survey sequence.	Homo sapiens	36,197	17-MAR-1999

Table 4 (continued)

rx02299	531	GB_EST23:AI128623	363	AI128623	qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2:ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
		GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9: AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
rx02311	813	GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97
rx02315	1752	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome: segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996
rx02318	402	GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
rx02319	1080	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome: segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
		GB_EST23:AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5', mRNA sequence.	Mus musculus	35,084	2-Sep-98

Table 4 (continued)

αa02345	1320	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99
αa02350	618	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
		GB_PL1:SC130KBXV	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
αa02373	1038	GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:106030	1853	106030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:100836	1853	100836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993
αa02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
αa02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
αa02382	1419	GB_BA1:CGPROAGE	1783	X82929	C.glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
αa02400	693	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:186191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
αa02432	1098	GB_GSS15:AQ60684	574	AQ606842	HS_5404_B2_E07_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99

Table 4 (continued)

rx02458	1413	GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDG63 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
		GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
		GB_GSS15:AQ65002	728	AQ650027	Sheared DNA-5L2, TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	39,281	22-Jun-99
		GB_BA1:MTCY359	36021	Z83859	Sheared DNA-5L2, genomic survey sequence.			
rx02469	1554	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.			
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Mycobacterium leprae	59,343	27-Aug-99
rx02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Streptomyces coelicolor	48,899	17-Sep-98
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:SOE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Mycobacterium tuberculosis	59,429	17-Jun-98
rx02499	933	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene; complete cds.	Streptomyces coelicolor	39,510	10-MAY-1999
		GB_BA1:NG17PILA	1920	X13965	Neisseria gonorrhoeae pilA gene.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_HTG2:AC007984	129715	AC007984	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp. *** SEQUENCING IN PROGRESS	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Drosophila melanogaster	33,406	2-Aug-99
rx02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.			
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_VI:HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome.	Mycobacterium leprae	51,768	01-MAR-1994
rx02503	522	GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	human herpesvirus 1	39,378	17-Apr-97
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	3-Sep-98
rx02504	681	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Homo sapiens	34,911	28-Jul-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	28-Jul-98
rx02516	1386	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Homo sapiens	41,265	3-Sep-98
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,723	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,723	01-MAR-1994

Table 4 (continued)

αa02517	570	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	61,335	17-Jun-98
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,018	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,018	01-MAR-1994
		GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	37,071	12-Jul-99
αa02532	1170	GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mli) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
αa02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAll project).	Arabidopsis thaliana	35,063	24-Feb-99
αa02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSGGB1970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
αa02559	1026	GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT:128684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown.	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
αa02622	1683	GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
αa02623	714	GB_GSS5:AQ818728	444	AQ818728	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence.	Homo sapiens	38,801	26-Aug-99
		GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_TTA RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99

Table 4 (continued)

rx02629	708	GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial 37,013 virus	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial 37,013 virus	28-Apr-93
rx02645	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
rx02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
rx02648	1326	GB_OV:ICTCNC	2049	M83111	Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictalurus punctatus	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5' mRNA sequence.	Mus musculus	20-MAR-1997
rx02653		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14. TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	27-Jun-98
rx02687	1068	GB_BA1:CORPHEA	1088	M13774	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
		GB_PAT:E06110	948	E06110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
rx02717	1005	GB_PL1:HVCH4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	25-MAR-1999
		GB_PR2:HS310H5	29718	Z69705	Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Homo sapiens	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	28-MAY-1998
rx02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPC1:98 16.1.18 map 95A-95A sifrai y, cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	37,838	10-Feb-99
GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	35,331	5-Nov-99
GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	33,807	5-Nov-99
GB_BA2:AF064070	23183	AF064070	Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apah), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Burkholderia pseudomallei	36,929	20-Jan-99
GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
GB_IN1:CELT1984	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA: Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP-C25D7.8 CE08394.; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998

Table 4 (continued)

rxs02814	494	GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394.; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PRI:HSJA2962	778	AJ002962	Homo sapiens mRNA for hB-FABP.	Homo sapiens	39,826	8-Jan-98
rxs02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS.	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	39,626	09-MAR-1995
rxs03205	963	GB_BA1:BLSIGBGN	2906	Z49824	B.lactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	88,854	25-Apr-96
		GB_EST21:AA980237	377	AA980237	ua32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN.; mRNA sequence.	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI158316	371	AI158316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5' mRNA sequence.	Mus musculus	38,005	30-Sep-98
rxs03223	1237	GB_IN1:LMFL2743	38368	AL031910	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	39,869	15-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,930	17-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,634	17-DEC-1999

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

25

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is selected from the group consisting of proteins involved in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

- 5 7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 10 8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous
15 polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
20
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 25 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
30
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine

bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12
5 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.
20. An isolated polypeptide comprising an amino acid sequence selected from the group
15 consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
21. An isolated polypeptide comprising a naturally occurring allelic variant of a
20 polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a
30 nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,
5 provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
10
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of
15 transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
20
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
25 *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
- 30
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 1156 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid

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modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of
5 the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing , wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

10

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
 <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 METABOLIC PATHWAY PROTEINS
 <130> BGI-121CPPC
 <140>
 <141>
 <160> 1156

<210> 1
 <211> 948
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(925)
 <223> RXA02229

<400> 1
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 aagccttgga gattttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115
 Leu Thr Ile Pro Phe
 1 5
 gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163
 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
 10 15 20
 gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211
 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
 25 30 35
 cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259
 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
 40 45 50
 gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307
 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
 55 60 65
 tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg 355
 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
 70 75 80 85
 cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403
 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
 90 95 100
 agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451
 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
 105 110 115
 cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499
 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
 120 125 130
 gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547
 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala

135	140	145	
ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg			595
Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro			
150	155	160	165
ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg			643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr			
	170	175	180
ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca			691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr			
	185	190	195
gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg			739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val			
	200	205	210
ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct			787
Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala			
	215	220	225
gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt			835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val			
	230	235	240
cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc			883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu			
	250	255	260
acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc			925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile			
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Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
 35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
 50 55 60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
 65 70 75 80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
 85 90 95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
 100 105 110
 His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
 115 120 125
 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
 130 135 140
 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
 145 150 155 160
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
 165 170 175
 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
 180 185 190
 Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val
 195 200 205
 Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
 210 215 220
 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
 225 230 235 240
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 Val Gln Ile
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 <223> RXS02970

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 Leu Ala Leu Lys Gly
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 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
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230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

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 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

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 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

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 1363
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 410 415 420

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 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
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<213> Corynebacterium glutamicum

<400> 4

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
          50           55           60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65           70           75           80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
          85           90           95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
          100          105          110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
          115          120          125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
          130          135          140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
          145          150          155          160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
          165          170          175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
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Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
          195          200          205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
          210          215          220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
          225          230          235          240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
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Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
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Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
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Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
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Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
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Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
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 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
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 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
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 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
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 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

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 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
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 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

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 1330
 Phe Lys Glu Arg Gly
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 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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 <223> RXC02390

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 Val Glu Trp Thr Ala
 1 5
 ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163
 Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
 10 15 20
 cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211
 Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
 25 30 35
 gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
 40 45 50
 acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
 55 60 65
 att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
 70 75 80 85
 ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
 90 95 100
 cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg_gat gcg gta gaa 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
 105 110 115
 gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130
 ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145
 ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165

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gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg      691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
                185                      190                      195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg      739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
                200                      205                      210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct      789
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<213> Corynebacterium glutamicum

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                20                      25                      30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
                35                      40                      45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
  50                      55                      60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
  65                      70                      75                      80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
                85                      90                      95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
                100                      105                      110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
                115                      120                      125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
  130                      135                      140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
  145                      150                      155                      160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
                165                      170                      175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
                180                      185                      190

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Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
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 Leu Leu Leu Gly Gly
 1 5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163
 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
 10 15 20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211
 Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
 25 30 35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
 Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
 40 45 50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307
 Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
 55 60 65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa 355
 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70 75 80 85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
 90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
 105 110 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
 120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595

Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
 150 155 160 165
 ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643
 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
 170 175 180
 ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
 185 190 195
 gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
 200 205 210
 tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag 787
 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
 215 220 225
 cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
 230 235 240 245
 gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884
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 cttttcgacg tct 897

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<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

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 35 40 45
 Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
 50 55 60
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125
 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu

130		135		140
Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn				
145		150		155 160
Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala				
	165		170	175
Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu				
	180		185	190
Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp				
	195		200	205
Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr				
	210		215	220
His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn				
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Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn				
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Asp Ala

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXC01207

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 Val Ser Arg Ile Tyr
 1 5
 gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
 10 15 20
 gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
 25 30 35
 tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
 40 45 50
 ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
 55 60 65
 ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355

Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70 75 80 85
 gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
 90 95 100
 gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
 105 110 115
 acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
 120 125 130
 cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
 135 140 145
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
 150 155 160 165
 gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180
 acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195
 gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa * 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
 200 205 210
 agc ctg cgc taaatgggag tcggtttcgc ggg 771
 Ser Leu Arg
 215

<210> 12

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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 20 25 30
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
 195 200 205

Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 13
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXC00657

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 Met Ser Thr Glu Asp
 1 5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
 10 15 20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211
 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
 25 30 35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
 40 45 50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307
 Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
 55 60 65

att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag 355
 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys 85
 70 75 80

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403
 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu 100
 90 95

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451
 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly 115
 105 110

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499
 Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser 130
 120 125

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547
 His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn 145
 135 140

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
 Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu 165
 150 155 160

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643
 Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg 180
 170 175

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag 691
 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln 195
 185 190

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
 Ala Ser Leu Ala Gly Leu Ala Ala Gln Gln Gln Trp Asp Glu Val 210
 200 205

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787
 Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val 225
 215 220

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg 245
 230 235 240

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val 260
 250 255

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser 275
 265 270

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val 290
 280 285

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 1026
 Arg Pro Pro Glu Lys Ile Lys Lys
 295 300

<210> 14
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 14

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Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
      35           40           45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
      50           55           60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65           70           75           80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
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Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
      100           105           110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
      115           120           125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130           135           140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145           150           155           160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
          165           170           175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
      180           185           190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
      195           200           205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210           215           220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225           230           235           240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
          245           250           255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
      260           265           270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
      275           280           285

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Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
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 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXC00552

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 Val Ala Thr Ser Lys
 1 5
 att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
 10 15 20
 cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
 25 30 35
 atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
 40 45 50
 gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
 55 60 65
 aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355
 Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
 70 75 80 85
 aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403
 Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
 90 95 100
 gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451
 Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
 105 110 115
 ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499
 Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
 120 125 130
 gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547
 Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
 135 140 145
 ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc 595
 Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
 150 155 160 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg 643
 Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
 170 175 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691
 Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
 185 190 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739
 Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
 200 205 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787
 Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
 215 220 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835
 Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
 230 235 240 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883
 Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
 250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
 280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc
 1027
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
 295 300 305

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 1059
 Val Thr Ser
 310

<210> 16
 <211> 312
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 35 40 45
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
 100 105 110
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
 145 150 155 160
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
 165 170 175
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
 195 200 205
 Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
 210 215 220
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
 225 230 235 240
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
 245 250 255
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
 260 265 270
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
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 Gly Ile Asp Pro Leu Val Thr Ser
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<210> 17

<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1555)

<223> RXN00351

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	Met Asp Asp Ser Asn	
	1 5	
agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac	163	
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His		
	10 15 20	
cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg	211	
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr		
	25 30 35	
ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg	259	
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp		
	40 45 50	
cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt	307	
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly		
	55 60 65	
gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc	355	
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe		
	70 75 80 85	
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg	403	
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu		
	90 95 100	
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag	451	
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu		
	105 110 115	
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt	499	
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly		
	120 125 130	
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att	547	
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile		
	135 140 145	
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att	595	
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile		
	150 155 160 165	
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag	643	
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu		
	170 175 180	
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt	691	
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val		
	185 190 195	
caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act	739	
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr		
	200 205 210	
gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa	787	
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu		
	215 220 225	

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835
 Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg
 230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883
 Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe
 250 255 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac 931
 Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp
 265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979
 Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys
 280 285 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc
 1027
 Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly
 295 300 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg
 1075
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser
 310 315 320 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa
 1123
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
 330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg
 1171
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
 345 350 355

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 <213> Corynebacterium glutamicum

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Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
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Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
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Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
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His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
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Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
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 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
 210 215 220
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
 225 230 235 240
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
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 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
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 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
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 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
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<213> Corynebacterium glutamicum

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<222> (101)..(1546)

<223> FRXA00351

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Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His
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Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu
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gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt 499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly
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Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile
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Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile
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ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag 643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu
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Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu	
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Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg	
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Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe	
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Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp	
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Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys	
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 Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
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<212> PRT

<213> *Corynebacterium glutamicum*

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Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
 35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
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Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
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Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
 85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
 100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
 115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
 130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
 145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
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 Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
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 Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
 195 200 205
 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
 210 215 220
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
 225 230 235 240
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
 245 250 255
 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
 260 265 270
 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
 275 280 285
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 305 310 315 320
 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
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 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
 340 345 350
 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
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 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
 370 375 380
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 435 440 445
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Ser Gly

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 <223> RXA00873

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 Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
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 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
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 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
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 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
 115 120 125
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 Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
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Ala	Glu	Arg	Glu	Trp	Ile	Val	Thr	Leu	Ala	Pro	His	Gly	Phe	Phe	Trp						
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 <213> Corynebacterium glutamicum

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 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
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 Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
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 Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
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 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
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 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
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 Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
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 Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
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 Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
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 Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn

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Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile		
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Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu		
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<220>
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 <223> RXA00891

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 Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val 35
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 Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro 50
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 Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp Glu Lys Lys Asn Arg 65
 55 60 65
 gag tgg tac aaa gac gcc gtt ttc tac gaa gtg ctg gtt cgt gcc ttc 355
 Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val Leu Val Arg Ala Phe 85
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 Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu Lys Gly Leu Thr Glu 100
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 aaa ctg gat tac atc cag tgg ctc ggc gtg gat tgc att tgg atc cca 451
 Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp Cys Ile Trp Ile Pro 115
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Phe	Arg	Glu	Ile	Leu	Pro	Glu	Phe	Gly	Thr	Val	Asp	Asp	Phe	Val	Glu		
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ctc	ggt	gac	cac	gcc	cac	cgc	cgt	ggc	ctg	cgt	ggt	atc	acc	gac	ttg	595	
Leu	Val	Asp	His	Ala	His	Arg	Arg	Gly	Leu	Arg	Val	Ile	Thr	Asp	Leu		
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cgc	gac	cca	acc	ggc	ccc	tac	gga	gat	ttc	tat	gtg	tgg	agc	gat	gat	691	
Arg	Asp	Pro	Thr	Gly	Pro	Tyr	Gly	Asp	Phe	Tyr	Val	Trp	Ser	Asp	Asp		
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Pro	Thr	Leu	Tyr	Asn	Glu	Ala	Arg	Ile	Ile	Phe	Val	Asp	Thr	Glu	Glu		
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Phe	Phe	Ser	His	Gln	Pro	Asp	Leu	Asn	Tyr	Asp	Asn	Pro	Ala	Val	Gln		
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Gly	Phe	Arg	Leu	Asp	Ala	Val	Pro	Tyr	Leu	Phe	Glu	Arg	Glu	Gly	Thr		
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Asn	Gln	Trp	Pro	Gln	Asp	Val	Val	Glu	Tyr	Phe	Gly	Glu	Lys	Asp	Lys		
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Gly	Asp	Glu	Cys	His	Met	Ala	Phe	His									
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<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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 1 5 10 15

Thr Ser Pro Leu Asn Ser Gln Pro Ser Ala Asp His His Pro Asp His
 20 25 30

Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu
 35 40 45

Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp
 50 55 60

Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val
 65 70 75 80

Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu
 85 90 95

Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp
 100 105 110

Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly
 115 120 125

Tyr Asp Ile Arg Asn Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val
 130 135 140

Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg
 145 150 155 160

Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp
 165 170 175

Phe Gln Glu Ser Arg Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr
 180 185 190

Val Trp Ser Asp Asp Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe
 195 200 205

Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln
 210 215 220

Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp
 225 230 235 240

Asn Pro Ala Val Gln Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu
 245 250 255

Asp Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe
 260 265 270

Glu Arg Glu Gly Thr Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe
 275 280 285

Leu Lys Leu Cys Arg Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile
 290 295 300

Leu Leu Ala Glu Ala Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe
305 310 315 320

Gly Glu Lys Asp Lys Gly Asp Glu Cys His Met Ala Phe His
325 330

<210> 25

<211> 1386

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA00534

<400> 25

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gcgggtaact gtcagcacgt agatcgaaag gtgcacaaag gtg gcc ctg gtc gta 115
Val Ala Leu Val Val
1 5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
10 15 20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
25 30 35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
40 45 50

gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
55 60 65

ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
70 75 80 85

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 403
Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
90 95 100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451
Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
105 110 115

cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt 499
Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
120 125 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547
Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
135 140 145

ggg cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg 595

Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	
150					155					160					165	
aac	gct	gat	gtg	tgt	gag	att	tac	tcg	gac	gtt	gac	ggt	gtg	tat	acc	643
Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	
				170					175					180		
gct	gac	ccg	cgc	atc	gtt	cct	aat	gca	cag	aag	ctg	gaa	aag	ctc	agc	691
Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	
			185					190					195			
ttc	gaa	gaa	atg	ctg	gaa	ctt	gct	gct	gtt	ggc	tcc	aag	att	ttg	gtg	739
Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	
		200					205					210				
ctg	cgc	agt	gtt	gaa	tac	gct	cgt	gca	ttc	aat	gtg	cca	ctt	cgc	gta	787
Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	
	215					220					225					
cgc	tcg	tct	tat	agt	aat	gat	ccc	ggc	act	ttg	att	gcc	ggc	tct	atg	835
Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu	Ile	Ala	Gly	Ser	Met	
230					235					240					245	
gag	gat	att	cct	gtg	gaa	gaa	gca	gtc	ctt	acc	ggt	gtc	gca	acc	gac	883
Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp	
				250					255					260		
aag	tcc	gaa	gcc	aaa	gta	acc	gtt	ctg	ggt	att	tcc	gat	aag	cca	ggc	931
Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile	Ser	Asp	Lys	Pro	Gly	
			265					270					275			
gag	gct	gcg	aag	gtt	ttc	cgt	gcg	ttg	gct	gat	gca	gaa	atc	aac	att	979
Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	
		280					285					290				
gac	atg	gtt	ctg	cag	aac	gtc	tct	tct	gta	gaa	gac	ggc	acc	acc	gac	
1027																
Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp	
	295					300					305					
atc	acc	ttc	acc	tgc	cct	cgt	tcc	gac	ggc	cgc	cgc	gcg	atg	gag	atc	
1075																
Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg	Arg	Ala	Met	Glu	Ile	
310					315					320					325	
ttg	aag	aag	ctt	cag	gtt	cag	ggc	aac	tgg	acc	aat	gtg	ctt	tac	gac	
1123																
Leu	Lys	Lys	Leu	Gln	Val	Gln	Gly	Asn	Trp	Thr	Asn	Val	Leu	Tyr	Asp	
				330					335					340		
gac	cag	gtc	ggc	aaa	gtc	tcc	ctc	gtg	ggt	gct	ggc	atg	aag	tct	cac	
1171																
Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala	Gly	Met	Lys	Ser	His	
			345					350					355			
cca	ggt	gtt	acc	gca	gag	ttc	atg	gaa	gct	ctg	cgc	gat	gtc	aac	gtg	
1219																
Pro	Gly	Val	Thr	Ala	Glu	Phe	Met	Glu	Ala	Leu	Arg	Asp	Val	Asn	Val	
		360					365					370				

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc
1267

Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc
1315

Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
390 395 400 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc
1363

Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
410 415 420

taaagtttta aaggagtagt ttt
1386

<210> 26

<211> 421

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 26

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
 420

<210> 27

<211> 1155

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00533

<400> 27

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 caggcaccgg acgctaaagt tttaaaggag tagttttaca atg acc acc atc gca 115
 Met Thr Thr Ile Ala

1															5		
ggt	ggt	ggt	gca	acc	ggc	cag	gtc	ggc	cag	ggt	atg	cgc	acc	ctt	ttg	163	
Val	Val	Gly	Ala	Thr	Gly	Gln	Val	Gly	Gln	Val	Met	Arg	Thr	Leu	Leu		
10					15					20							
gaa	gag	cgc	aat	ttc	cca	gct	gac	act	ggt	cgt	ttc	ttt	gct	tcc	cca	211	
Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	Phe	Phe	Ala	Ser	Pro		
25					30					35							
cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	acg	gaa	atc	gag	gta	259	
Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	Thr	Glu	Ile	Glu	Val		
40					45					50							
gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	aag	gac	atc	gac	ggt	307	
Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val		
55					60					65							
gcg	ttg	ttc	tcc	gct	gga	ggc	acc	gct	tcc	aag	cag	tac	gct	cca	ctg	355	
Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu		
70					75					80					85		
ttc	gct	gct	gca	ggc	gcg	act	ggt	gtg	gat	aac	tct	tct	gct	tgg	cgc	403	
Phe	Ala	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn	Ser	Ser	Ala	Trp	Arg		
90					95					100							
aag	gac	gac	gag	ggt	cca	cta	atc	gtc	tct	gag	gtg	aac	cct	tcc	gac	451	
Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp		
105					110					115							
aag	gat	tcc	ctg	gtc	aag	ggc	att	att	gcg	aac	cct	aac	tgc	acc	acc	499	
Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr		
120					125					130							
atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt	547	
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu		
135					140					145							
gta	aag	ctt	cac	ggt	tcc	tct	tac	cag	gct	ggt	tcc	ggt	tct	ggt	ctt	595	
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu		
150					155					160					165		
gca	ggt	gtg	gaa	acc	ttg	gca	aag	cag	ggt	gct	gca	ggt	gga	gac	cac	643	
Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His		
170					175					180							
aac	ggt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc	691	
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val		
185					190					195							
gga	cct	tat	ggt	tca	cca	atc	gct	tac	aac	gtg	ctg	cca	ttc	gcc	gga	739	
Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	Leu	Pro	Phe	Ala	Gly		
200					205					210							
aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gat	gaa	gag	cag	aag	ctg	787	
Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	Glu	Glu	Gln	Lys	Leu		
215					220					225							
cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggt	ctc	cca	gac	ctc	aag	gtc	tca	835	
Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	Asp	Leu	Lys	Val	Ser		
230					235					240					245		

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ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att      883
Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
                250                      255                      260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc      931
His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
                265                      270                      275

ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt      979
Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
                280                      285                      290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac
1027
Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
                295                      300                      305

tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac
1075
Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
310                      315                      320                      325

aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg
1123
Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
                330                      335                      340

ctg gtt aag taaaaacccg ccattaaaaa ctc
1155
Leu Val Lys

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<210> 28
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

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Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
                35                40                45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
                50                55                60

Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
                65                70                75                80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
                85                90                95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
                100                105                110

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Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
 115 120 125
 Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
 130 135 140
 Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
 145 150 155 160
 Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
 165 170 175
 Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
 180 185 190
 Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
 195 200 205
 Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
 210 215 220
 Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
 225 230 235 240
 Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
 245 250 255
 His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
 260 265 270
 Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
 275 280 285
 Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
 290 295 300
 Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
 305 310 315 320
 Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
 325 330 335
 Gln Ile Ala Glu Leu Leu Val Lys
 340

<210> 29

<211> 608

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 29

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 tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

1	5	10	
acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac			158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp			
15	20	25	30
cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc			206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val			
	35	40	45
acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc			254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr			
	50	55	60
gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt			302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val			
	65	70	75
ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac			350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn			
	80	85	90
aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca			398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala			
	95	100	105
ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc			446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser			
	115	120	125
gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg			494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val			
	130	135	140
cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat			542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp			
	145	150	155
ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg			590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr			
	160	165	170
ctc ggc gct tcc atg gtt			608
Leu Gly Ala Ser Met Val			
175	180		

<210> 30

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly			
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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser			
	20	25	30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg			
	35	40	45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160
 Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175
 Ala Ser Met Val
 180

<210> 31
 <211> 1230
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1207)
 <223> RXA02022

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 Val Asn Ser Glu Leu 5
 1
 aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg 20
 10 15
 ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat 211
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp 35
 25 30 35
 gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val 50
 40 45 50
 ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307
 Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala 65
 55 60 65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
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Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
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Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
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Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
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cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
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Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
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ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
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Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
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Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
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Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
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Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
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Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
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1123

Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
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1171

Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
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Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
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Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
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Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
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His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
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Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
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Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
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Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
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Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
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Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
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Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
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Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
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Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
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Phe	Leu	Thr	Arg	Ala	Gln	Arg	Lys	Leu	Ala	Leu	Thr	Thr	Ile	Ile	Glu	
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Glu	Gly	Leu	Val	Ala	Thr	Ala	Pro	Phe	Tyr	Thr	Arg	Thr	His	Asp	Val	
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Glu	Ile	Glu	Glu	His	Phe	Arg	Lys	Ile	His	Ala	Ala	Ala	Pro	Glu	Leu	
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Leu	Cys	Leu	Asp	Gly	Lys	Trp	Ala	Glu	Ala	Ala	Ala	Leu	Gln	Lys	Arg	
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atc	aac	cac	ctc	ttc	cac	atc	gtc	ttc	gtg	gga	gac	acc	tcc	cat	atg	883
Ile	Asn	His	Leu	Phe	His	Ile	Val	Phe	Val	Gly	Asp	Thr	Ser	His	Met	

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 Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
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 ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979
 Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
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 agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg
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 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
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 Tyr Thr Ala
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 Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
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 Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
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 Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
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 Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
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 Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
 130 135 140
 His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
 145 150 155 160
 Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
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 Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys

180	185	190
Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly 195 200 205		
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Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys 260 265 270		
Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val 275 280 285		
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ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307 Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn 55 60 65		
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Leu	Ile	Ala	Pro	Asn	Phe	Ala	Ile	Ser	Ala	Val	Leu	Thr	Met	Val	Phe	
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cac	cac	ccc	aac	aag	ctg	gat	gca	cct	tca	ggc	acc	gcg	atc	cac	act	547
His	His	Pro	Asn	Lys	Leu	Asp	Ala	Pro	Ser	Gly	Thr	Ala	Ile	His	Thr	
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Asp	Ser	Tyr	Asp	Arg	Asn	Ser	Phe	Ala	Pro	Gly	Val	Leu	Val	Gly	Val	
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<213> Corynebacterium glutamicum

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Glu	Ile	Gly	Val	Asp	Asp	Asp	Leu	Ser	Leu	Leu	Val	Asp	Asn	Gly	Ala	
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Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys		
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Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val		
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Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala		
	115	120 125
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly		
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Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala		
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Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser		
	165	170 175
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser		
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Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly		
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Thr	Ala	Ser	Asn	Ala	Ala	Tyr	Leu	Arg	His	Ile	Met	Glu	Val	Gly	His		
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Thr	Ala	Leu	Leu	Glu	His	Ala	Asn	Ala	Thr	Met	Tyr	Ile	Arg	Gly	Ile		
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Tyr	Val	Met	Asp	Phe													
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Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
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Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

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<210> 39
<211> 608
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 39

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tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
      Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
        1             5             10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
  15             20             25             30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
              35             40             45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
              50             55             60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
        65             70             75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
  80             85             90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
  95             100             105             110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
              115             120             125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
        130             135             140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
        145             150             155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
        160             165             170

ctc ggc gct tcc atg gtt
Leu Gly Ala Ser Met Val
175             180

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<210> 40

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
      35             40             45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
      50             55             60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
      65             70             75             80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
      85             90             95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
      100            105            110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
      115            120            125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
      130            135            140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
      145            150            155            160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
      165            170            175

Ala Ser Met Val
      180

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<210> 41

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN00355

<400> 41

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ggtcctgatg aaagagatgt ccctgaatca tcacctaagt atg cat ctc ggt aag 115
              Met His Leu Gly Lys
              1             5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
      10             15             20

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acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc	211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser	
25 30 35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc	259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile	
40 45 50	
ttc tgc cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc	307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val	
55 60 65	
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc	355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys	
70 75 80 85	
atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210	
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc	931

Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
265 270 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979
Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe
280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag
1027

Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac
1075

Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc
1120

Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
330 335 340

taatttagct cgaggggcaa gga
1143

<210> 42
<211> 340
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 42

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
 275 280 285
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
 290 295 300
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
 305 310 315 320
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335
 Ala Arg Asp Val
 340

<210> 43
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> FRXA00352

<400> 43
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 ggtcctgatg aaagagatgt ccctgaatca tcacttaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20
 acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser

	25	30	35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc				259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile				
	40	45	50	
ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc				307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val				
	55	60	65	
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc				355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys				
	70	75	80	85
atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag				403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln				
	90	95	100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc				451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg				
	105	110	115	
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca				499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala				
	120	125	130	
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc				547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val				
	135	140	145	
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc				595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly				
	150	155	160	165
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc				643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly				
	170	175	180	
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa				691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu				
	185	190	195	
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac				739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His				
	200	205	210	
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc				787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile				
	215	220	225	
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc				835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val				
	230	235	240	245
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc				883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly				
	250	255	260	
atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc				931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe				
	265	270	275	

aac cac acc gtg gaa tac atc ctc aag
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

958

<210> 44

<211> 286

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 44

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
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Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
 20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly

260 265 270
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
 275 280 285

<210> 45
 <211> 1400
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1377)
 <223> RXA00972

<400> 45
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 1 5 10 15
 aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat 96
 Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
 20 25 30
 gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg 144
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
 35 40 45
 cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag 192
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
 50 55 60
 gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga 240
 Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65 70 75 80
 cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att 288
 Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
 85 90 95
 gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc 336
 Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
 100 105 110
 aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc 384
 Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
 115 120 125
 acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt 432
 Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
 130 135 140
 caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa 480
 Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
 145 150 155 160
 ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528
 Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
 165 170 175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc 576
 Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
 180 185 190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc 624
 Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
 195 200 205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg 672
 Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
 210 215 220

gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc 720
 Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
 225 230 235 240

ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac 768
 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
 245 250 255

agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac 816
 Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Tyr
 260 265 270

ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt 864
 Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
 275 280 285

gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc 912
 Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
 290 295 300

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc 960
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
 305 310 315 320

ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac
 1008
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335

gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg
 1056
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350

tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc
 1104
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
 355 360 365

gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg
 1152
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370 375 380

ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac
 1200
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400

cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc
 1248
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415

gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc
 1296
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
 420 425 430

gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc
 1344
 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
 435 440 445

gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga
 1397
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
 450 455

ccc
 1400

<210> 46
 <211> 459
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 46
 Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
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Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
 20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
 35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
 50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
 85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
 100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
 115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
 130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
 145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu

165										170					175				
Ile	Arg	Val	Lys	Pro	Gly	Ile	Glu	Ala	His	Thr	His	Glu	Phe	Ile	Ala				
			180					185					190						
Thr	Ser	His	Glu	Asp	Gln	Lys	Phe	Gly	Phe	Ser	Leu	Ala	Ser	Gly	Ser				
		195					200					205							
Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu	Asn	Leu				
	210					215					220								
Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala	Glu	Gly				
225					230					235					240				
Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	His				
				245					250					255					
Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly	Gly	Tyr				
			260					265					270						
Gly	Ile	Ala	Tyr	Thr	Ala	Ala	Glu	Glu	Pro	Leu	Asn	Val	Ala	Glu	Val				
	275						280					285							
Ala	Ser	Asp	Leu	Leu	Thr	Ala	Val	Gly	Lys	Met	Ala	Ala	Glu	Leu	Gly				
	290					295					300								
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Val	Asp	Asp	Asp	Lys	Thr	Arg	Arg	Tyr	Ile	Ala	Val	Asp	Gly	Gly	Met				
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Val	Val	Ser	Arg	Phe	Ala	Glu	Gly	Asp	Pro	Val	Ser	Thr	Arg	Ile	Val				
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Gly	Ser	His	Cys	Glu	Ser	Gly	Asp	Ile	Leu	Ile	Asn	Asp	Glu	Ile	Tyr				
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Pro	Ser	Asp	Ile	Thr	Ser	Gly	Asp	Phe	Leu	Ala	Leu	Ala	Ala	Thr	Gly				
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Ala	Tyr	Cys	Tyr	Ala	Met	Ser	Ser	Arg	Tyr	Asn	Ala	Phe	Thr	Arg	Pro				
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Ala	Val	Val	Ser	Val	Arg	Ala	Gly	Ser	Ser	Arg	Leu	Met	Leu	Arg	Arg				
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<222> (101)..(2098)

<223> RXA02653

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Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
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Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
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Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu
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Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu
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Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu
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Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His
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Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu
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Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro
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Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly
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caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg 691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu
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ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc 835
 Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu
 230 235 240 245

act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt 883
 Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser
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cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag 931
 Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu
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 Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val
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 Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile
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 Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val
 375 380 385

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 1363

Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His
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 Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe
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 Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro
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 1651
 Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser
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 1699
 Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile
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 1747
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
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 gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg
 1795
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
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 1843
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
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 1891
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
 585 590 595
 tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg
 1939
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg

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        600                605                610

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cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac
2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
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caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac
2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
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Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
      35                40                45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
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Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
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Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
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Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
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Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
      115                120                125

Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
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Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
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Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
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 195 200 205
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
 210 215 220
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
 225 230 235 240
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
 245 250 255
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
 260 265 270
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
 275 280 285
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
 290 295 300
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
 305 310 315 320
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
 325 330 335
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
 340 345 350
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
 355 360 365
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
 370 375 380
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
 385 390 395 400
 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
 420 425 430
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
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 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
 450 455 460
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
 465 470 475 480
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
 485 490 495

Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
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Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly
515 520 525

Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly
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Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu
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Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser
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Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly
580 585 590

Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu
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Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly
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Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu
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Met Asn Pro Ile Gln
1 5

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Leu Asp Thr Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
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Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
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Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro

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Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys			
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atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt			355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu			
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gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca			403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr			
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Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr			
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Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala			
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Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala			
	155	160	165
acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg			643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp			
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Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp			
	185	190	195
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Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val			
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Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly			
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Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys			
	230	235	240
gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg			883
Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met			
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Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr			
	265	270	275
gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc			980
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<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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Ser	Gln	Arg	Val	Lys	Ala	Leu	Glu	His	His	Val	Gly	Arg	Val	Leu	Val
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Ser	Arg	Thr	Gln	Pro	Ala	Lys	Ala	Thr	Glu	Ala	Gly	Glu	Val	Leu	Val
	50					55					60				

Gln	Ala	Ala	Arg	Lys	Met	Val	Leu	Leu	Gln	Ala	Glu	Thr	Lys	Ala	Gln
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Leu	Ser	Gly	Arg	Leu	Ala	Glu	Ile	Pro	Leu	Thr	Ile	Ala	Ile	Asn	Ala
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Trp	Gly	Gly	Ala	Thr	Leu	Thr	Leu	Arg	Leu	Glu	Asp	Glu	Ala	His	Thr
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Leu	Ser	Leu	Leu	Arg	Arg	Gly	Asp	Val	Leu	Gly	Ala	Val	Thr	Arg	Glu
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Ala	Asn	Pro	Val	Ala	Gly	Cys	Glu	Val	Val	Glu	Leu	Gly	Thr	Met	Arg
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His	Leu	Ala	Ile	Ala	Thr	Pro	Ser	Leu	Arg	Asp	Ala	Tyr	Met	Val	Asp
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Gly	Lys	Leu	Asp	Trp	Ala	Ala	Met	Pro	Val	Leu	Arg	Phe	Gly	Pro	Lys
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		195					200					205			

Gly	Arg	Arg	Arg	Val	Ser	Ile	Val	Pro	Ser	Ala	Glu	Gly	Phe	Gly	Glu
	210					215					220				

Ala	Ile	Arg	Arg	Gly	Leu	Gly	Trp	Gly	Leu	Leu	Pro	Glu	Thr	Gln	Ala
225					230					235					240

Ala	Pro	Met	Leu	Lys	Ala	Gly	Glu	Val	Ile	Leu	Leu	Asp	Glu	Ile	Pro
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Arg Pro
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 <223> RXA00241

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 Val Asn Thr Gln Ser
 1 5
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 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
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 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
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 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
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 Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr
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 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser
 120 125 130
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 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp
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Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu
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 Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp
 185 190 195
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 Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala
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 Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met
 310 315 320 325
 gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct
 1123
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
 330 335 340
 gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc
 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355
 atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg
 1219
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg
 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc
 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc
 1363
 Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
 410 415 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg
 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg
 1459
 Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa
 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
 455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt
 1555
 Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt
 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500

taaacaccga aaccttcctg cta
 1626

<210> 52

<211> 501

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 52

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
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Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
 20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
 35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 140
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
 180 185 190
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 220
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365
 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
 370 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
 385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
 405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
 420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
 435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
 450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
 465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
 485 490 495

Gly Ser Leu Ser Leu
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<210> 53
 <211> 822
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(799)
 <223> RXA01394

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 Met Glu Ile Phe Ile
 1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
 10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
 25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
 40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
 55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85

gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att 403
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
 90 95 100
 gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg 451
 Glu Glu Thr Glu Pro Thr Val Pro Asp Thr Pro Leu Gly Gly Ser
 105 110 115
 gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
 120 125 130
 gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg 547
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
 135 140 145
 acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 150 155 160 165
 ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct 643
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
 170 175 180
 ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc 691
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
 185 190 195
 gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg 739
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
 200 205 210
 atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787
 Ile Asn Val Val Val Ala Val Met Thr Ala Leu Ala Ile Lys Leu
 215 220 225
 atg ttg atg ggt tagtttttcgc gggtttttgga atc 822
 Met Leu Met Gly
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<210> 54

<211> 233

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 54

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Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
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Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
 35 40 45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala
 50 55 60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu

65	70	75	80
Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu	85	90	95
Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr	100	105	110
Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg	115	120	125
Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu	130	135	140
Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala	145	150	155
Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg	165	170	175
Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro	180	185	190
Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro	195	200	205
Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala	210	215	220
Leu Ala Ile Lys Leu Met Leu Met Gly	225	230	

<210> 55

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00865

<400> 55

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				Met	Ser	Thr	Gly	Leu	
				1				5	

aca	gct	aag	acc	gga	gta	gag	cac	ttc	ggc	acc	ggt	gga	gta	gca	atg	163
Thr	Ala	Lys	Thr	Gly	Val	Glu	His	Phe	Gly	Thr	Val	Gly	Val	Ala	Met	
				10					15				20			

ggt	act	cca	ttc	acg	gaa	tcc	gga	gac	atc	gat	atc	gct	gct	ggc	cgc	211
Val	Thr	Pro	Phe	Thr	Glu	Ser	Gly	Asp	Ile	Asp	Ile	Ala	Ala	Gly	Arg	
			25					30					35			

gaa	gtc	gcg	gct	tat	ttg	gtt	gat	aag	ggc	ttg	gat	tct	ttg	gtt	ctc	259
Glu	Val	Ala	Ala	Tyr	Leu	Val	Asp	Lys	Gly	Leu	Asp	Ser	Leu	Val	Leu	
		40					45					50				

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala	
120 125 130	
att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa	979
Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu	
280 285 290	

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattccccga aat
 1026
 Asp Met Lys Lys Ala Gly Val Leu
 295 300

<210> 56
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 56
 Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
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 Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
 20 25 30
 Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
 35 40 45
 Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
 50 55 60
 Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
 65 70 75 80
 Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
 85 90 95
 Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
 100 105 110
 Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
 115 120 125
 Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
 130 135 140
 Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
 145 150 155 160
 Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
 165 170 175
 Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
 180 185 190
 Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
 195 200 205
 Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
 210 215 220
 Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
 225 230 235 240
 Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
 245 250 255
 Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn

260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
290 295 300

<210> 57
 <211> 1071
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1048)
 <223> RXS02021

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 aaaccttagt taaaacatga tggaagcgggt cgattaaaaa atg agt gaa aac att 115
 Met Ser Glu Asn Ile 5
 cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
 Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr 20
 atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211
 Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln 35
 tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259
 Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala 50
 aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
 Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp 65
 cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355
 Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser 85
 caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403
 Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu 100
 tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
 Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu 115
 gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499
 Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro 130
 gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547
 Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

 ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

 tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

 aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

 ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

 cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

 caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

 gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

 ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag
 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

 cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc
 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 58

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35					40					45						
Thr	Arg	Leu	Gly	Ala	Asn	Glu	Leu	Thr	Pro	Arg	Met	Leu	Gln	Leu	Val	
50					55					60						
Lys	Leu	Asp	Gln	Asp	Arg	Leu	Val	Glu	Gln	Val	Ala	Val	Arg	Thr	Val	
65					70					75					80	
Ile	Pro	Asp	Leu	Ser	Gln	Pro	Pro	Val	Asp	Ala	His	Asp	Val	Tyr	Leu	
85					90					95						
Arg	Leu	His	Leu	Leu	Ser	His	Arg	Leu	Val	Arg	Pro	His	Glu	Met	His	
100					105					110						
Met	Gln	Asn	Thr	Leu	Glu	Leu	Leu	Ser	Asp	Val	Val	Trp	Thr	Asn	Lys	
115					120					125						
Gly	Pro	Cys	Leu	Pro	Glu	Asn	Phe	Glu	Trp	Val	Arg	Gly	Ala	Leu	Arg	
130					135					140						
Ser	Arg	Gly	Leu	Ile	His	Val	Tyr	Cys	Val	Asp	Arg	Leu	Pro	Arg	Met	
145					150					155					160	
Val	Asp	Tyr	Val	Val	Pro	Pro	Gly	Val	Arg	Ile	Ser	Glu	Ala	Glu	Arg	
165					170					175						
Val	Arg	Leu	Gly	Ala	Tyr	Leu	Ala	Pro	Gly	Thr	Ser	Val	Leu	Arg	Glu	
180					185					190						
Gly	Phe	Val	Ser	Phe	Asn	Ser	Gly	Thr	Leu	Gly	Ala	Ala	Lys	Val	Glu	
195					200					205						
Gly	Arg	Leu	Ser	Ser	Gly	Val	Val	Ile	Gly	Glu	Gly	Ser	Glu	Ile	Gly	
210					215					220						
Leu	Ser	Ser	Thr	Ile	Gln	Ser	Pro	Arg	Asp	Glu	Gln	Arg	Arg	Arg	Leu	
225					230					235					240	
Pro	Leu	Ser	Ile	Gly	Gln	Asn	Cys	Asn	Phe	Gly	Val	Ser	Ser	Gly	Ile	
245					250					255						
Ile	Gly	Val	Ser	Leu	Gly	Asp	Asn	Cys	Asp	Ile	Gly	Asn	Asn	Ile	Val	
260					265					270						
Leu	Asp	Gly	Asp	Thr	Pro	Ile	Trp	Phe	Ala	Ala	Asp	Glu	Glu	Leu	Arg	
275					280					285						
Thr	Ile	Asp	Ser	Ile	Glu	Gly	Gln	Ala	Asn	Trp	Ser	Ile	Lys	Arg	Glu	
290					295					300						
Ser	Gly	Phe	His	Glu	Pro	Val	Ala	Arg	Leu	Lys	Ala					
305					310					315						

<210> 59

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RXS02157

<400> 59

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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
                                         Met Ser Thr Leu Glu
                                         1                               5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
                               10                               15                               20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
                               25                               30                               35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
                               40                               45                               50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
                               55                               60                               65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu
                               70                               75                               80                               85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
                               90                               95                               100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
                               105                               110                               115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
                               120                               125                               130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
                               135                               140                               145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
                               150                               155                               160                               165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
                               170                               175                               180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
                               185                               190                               195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
                               200                               205                               210

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tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc
 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

atc gca taaaggactc aaacttatga ctt
 1296
 Ile Ala
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<210> 60

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
              20              25              30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
      35              40              45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
      50              55              60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
      65              70              75              80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
              85              90              95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
              100              105              110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
      115              120              125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
      130              135              140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
      145              150              155              160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
              165              170              175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
              180              185              190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
      195              200              205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
      210              215              220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
      225              230              235              240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
              245              250              255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
              260              265              270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
      275              280              285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
      290              295              300

Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
      305              310              315              320

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ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
 Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
 120 125 130

atc ggt agc ctg ttg tgc ttg ttc cag gcg cgg atg ctc aac cgc atc 547
 Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile
 135 140 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595
 Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile
 150 155 160 165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg 643
 His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu
 170 175 180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa 691
 Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln
 185 190 195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg 739
 Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val
 200 205 210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg 787
 Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu
 215 220 225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg
 230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn
 250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe
 265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979
 Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala
 280 285 290

tgt gta taaggccagc tttggtgccc agt
 1008
 Cys Val
 295

<210> 62

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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20										25					30				
Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe				
		35						40				45							
Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu				
		50				55					60								
Gly	Lys	Ala	Thr	Asn	Val	Val	Phe	Glu	Gly	Phe	Leu	Ser	Lys	Arg	Met				
		65			70					75					80				
Pro	Ala	Gly	Ala	Ser	Lys	Glu	Asp	Ile	Ile	Ala	Gln	Leu	Gln	Ala	Ala				
				85					90					95					
Gly	Lys	His	Asn	Gln	Ala	Ser	Met	Met	Glu	Asp	Met	Asn	Leu	Val	Pro				
			100					105					110						
Gly	Ser	Gly	Ile	Asp	Phe	Glu	Lys	Leu	Ala	Met	Ile	Leu	Gly	Leu	Val				
		115					120					125							
Ile	Gly	Ala	Tyr	Leu	Ile	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Gln	Ala	Arg				
		130				135						140							
Met	Leu	Asn	Arg	Ile	Val	Gln	Ser	Ala	Met	His	Arg	Leu	Arg	Met	Glu				
					150					155					160				
Val	Glu	Glu	Lys	Ile	His	Arg	Leu	Pro	Leu	Ser	Tyr	Phe	Asp	Ser	Ile				
				165					170					175					
Lys	Arg	Gly	Asp	Leu	Leu	Ser	Arg	Val	Thr	Asn	Asp	Val	Asp	Asn	Ile				
			180					185					190						
Gly	Gln	Ser	Leu	Gln	Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu				
		195					200					205							
Thr	Val	Ile	Gly	Val	Leu	Val	Met	Met	Phe	Ile	Ile	Ser	Pro	Leu	Leu				
		210				215						220							
Ala	Leu	Val	Ala	Leu	Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val				
		225			230					235				240					
Val	Val	Ala	Ser	Arg	Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln				
				245					250				255						
Thr	Gly	Ile	Leu	Asn	Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala				
			260					265					270						
Val	Val	Lys	Val	Phe	Gly	His	Gln	Lys	Asp	Val	Gln	Glu	Ala	Phe	Glu				
		275					280					285							
Glu	Glu	Asn	Gln	Ala	Cys	Val													
		290				295													

<210> 63

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(426)

<223> RXC00861

<400> 63

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 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc 96
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggg aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggg gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 64

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

His	Gly	Tyr	Ser	Gly	Glu	Leu	Leu	Phe	Leu	Tyr	Asn	Ala	Ala	Arg	Pro
				85					90					95	
Lys	Asn	Ala	Met	Pro	Val	His	Gly	Glu	Trp	Arg	His	Leu	Arg	Ala	Asn
			100					105					110		
Lys	Glu	Leu	Ala	Ile	Ser	Thr	Gly	Val	Asn	Arg	Asp	Asn	Val	Val	Leu
			115				120					125			
Ala	Gln	Asn	Gly	Val	Val	Val	Asp	Met	Val	Asn	Gly	Arg	Ala		
	130					135					140				

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<211> 1066
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (1066)
<223> RXC00866
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Met Asn Asp Ser Arg 5															
aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163															
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly 20															
cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211															
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser 35															
tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259															
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg 50															
gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307															
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln 65															
aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355															
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn 85															
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403															
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly 100															
aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451															
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln 115															
ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499															
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys															

120	125	130	
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag			547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys			
135	140	145	
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa			595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu			
150	155	160	165
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc			643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile			
170	175		180
gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac			691
Val Asp Cys Gly Val Leu Phe Pro Ser Gly Glu Pro Gly Val Asp			
185	190		195
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc			739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val			
200	205		210
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att			787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile			
215	220		225
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt			835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg			
230	235	240	245
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt			883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg			
250	255		260
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg			931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro			
265	270		275
ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt			979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu			
280	285		290
ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac			
1027			
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp			
295	300	305	
atc aag ctg gat cag act cct cct gat gga cgc cca act			
1066			
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr			
310	315	320	
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<211> 322			
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<400> 66			
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 Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala
 35 40 45
 Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp
 50 55 60
 Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65 70 75 80
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
 85 90 95
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
 100 105 110
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
 290 295 300
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
 305 310 315 320
 Pro Thr


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<220>  
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<222> (101) .. (1504)  
<223> RXC02095
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tactccccc acaggetcaa aaatactgaa aggctcacgc															115
Met Lys Thr Glu Gln															5
tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa															163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln															20
cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc															211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr															35
tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca															259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr															50
ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc															307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr															65
gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga															355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly															85
tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg															403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu															100
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc															451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu															115
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg															499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu															130
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta															547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val															145
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg															595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala															165
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg															643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu															180

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg	691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val	
185 190 195	
ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt	739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu	
200 205 210	
ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act	787
Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr	
215 220 225	
cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg	835
His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala	
230 235 240 245	
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta	883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu	
250 255 260	
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc	931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro	
265 270 275	
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc	979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly	
280 285 290	
ggg ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg	
1027	
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val	
295 300 305	
gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg	
1075	
Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu	
310 315 320 325	
tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc	
1123	
Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg	
330 335 340	
atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac	
1171	
Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His	
345 350 355	
ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta	
1219	
Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val	
360 365 370	
gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt	
1267	
Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly	
375 380 385	
gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct	
1315	

Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala
 390 395 400 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc
 1363

Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala
 410 415 420

ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc
 1411

Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser
 425 430 435

gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac
 1459

Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr
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tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag
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Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln
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tgatgagcag atcgaacacg cag
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<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val

145		150		155		160
Gln Ser Leu Val	Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys					
	165			170		175
Leu Val Leu Thr	Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr					
	180		185			190
Ile Ile Ala Ala	Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr					
	195		200			205
Ser Arg Lys Ala	Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala					
	210		215			220
Ala Asp Leu Thr	Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val					
	225		230			235
Val Lys Ala Phe	Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu					
	245		250			255
Thr Ala Arg Glu	Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr					
	260		265			270
Ala Lys Phe Ile	Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val					
	275		280			285
Val Asn Ile Val	Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr					
	290		295			300
Val Gly Thr Phe	Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala					
	305		310			315
Val Ala Arg Ser	Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu					
	325		330			335
Ser Ser Val Glu	Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg					
	340		345			350
Thr Asp Pro Ala	His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu					
	355		360			365
Ser Phe Asn Asn	Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu					
	370		375			380
Gly Val Gln Ala	Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser					
	385		390			395
Gly Lys Thr Met	Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp					
	405		410			415
Ser Gly His Ile	Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp					
	420		425			430
Asp Leu Thr His	Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp					
	435		440			445
Glu Pro Phe Leu	Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly					
	450		455			460
Phe Gly Cys Gln						
465						

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                Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
                  1                      5                      10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
                  15                      20                      25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
                  30                      35                      40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
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Ser Arg Glu Ser Leu
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Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
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                                         Met Lys Pro Gln Gly
                                         1                               5

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
                               10                               15                               20

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
                               25                               30                               35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
                               40                               45                               50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
                               55                               60                               65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
                               70                               75                               80                               85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
                               90                               95                               100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
                               105                               110                               115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
                               120                               125                               130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
                               135                               140                               145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
                               150                               155                               160                               165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
                               170                               175                               180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
                               185                               190                               195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu

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tcg gcc att gct att gtg cac	tcg cgt ttc tcc acg aac act ttc cca		787
Ser Ala Ile Ala Ile Val His	Ser Arg Phe Ser Thr Asn Thr Phe Pro		
215	220	225	
agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag			835
Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu			
230	235	240	245
atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg			883
Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala			
250	255	260	
ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc			931
Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile			
265	270	275	
tgc acc ccg gag ggc tgc gat acc gcg cgt ttc gac gag gct ttg gag			979
Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu			
280	285	290	
ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg			
1027			
Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met			
295	300	305	
atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt			
1075			
Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg			
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gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct			
1123			
Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro			
330	335	340	
gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac			
1171			
Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp			
345	350	355	
cgt aat ggc ctg cga cct ggg cga atc acc att act gat tgc ggt ttg			
1219			
Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu			
360	365	370	
gtt gtg atg gct tct gaa tgc gga gtg ttg gac ttg agg gag gag agc			
1267			
Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser			
375	380	385	
gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac			
1315			
Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp			
390	395	400	405
act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta			
1363			
Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu			
410	415	420	

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 425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt
 1459
 Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg
 440 445 450

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 Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp
 455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc
 1555
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 470 475 480 485

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 1603
 Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
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 1651
 Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
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 1699
 Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
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 Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
 535 540 545

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 1795
 Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
 550 555 560 565

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 1843
 Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
 570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct
 1891
 Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
 585 590 595

gcg att gct cgt gtg cgc cgc gag gtt tct gaa gca atc cgc aat ggc
 1939
 Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu Ala Ile Arg Asn Gly
 600 605 610

aag acg ttg atc gtg ctg tcg gat cgt gaa tct gat gag cgc atg gca
1987
Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser Asp Glu Arg Met Ala
615 620 625

cct atc cct gcg ctg ctg ctg act tcc gct gtg cat cag tac ttg gtg
2035
Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val His Gln Tyr Leu Val
630 635 640 645

cag caa cgt acc cgt acc cag tgc tcc ctg gtg gtg gaa tcc ggc gat
2083
Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val Val Glu Ser Gly Asp
650 655 660

gcc cgc gag gtt cat cac ctg gcg atg ctc att ggt ttt ggt gcc gat
2131
Ala Arg Glu Val His His Leu Ala Met Leu Ile Gly Phe Gly Ala Asp
665 670 675

gcg atc aac ccg tac atg gca ttt gaa acc atc gat gag ctg cgc atg
2179
Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile Asp Glu Leu Arg Met
680 685 690

aag ggt cag ttg ggt gat ctt tct ttg gat gag gca tcc cga aac tac
2227
Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu Ala Ser Arg Asn Tyr
695 700 705

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2275
Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val Met Ser Lys Met Gly
710 715 720 725

att gca acg gtg tct tcg tac cgt ggc gcg cag ctt gcc gat gtc act
2323
Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln Leu Ala Asp Val Thr
730 735 740

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2371
Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe Gly Gly Ile Ala Ser
745 750 755

cca att tct ggc atc ggt ctg gat gaa gtt gca gct gac gta gaa gct
2419
Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala Ala Asp Val Glu Ala
760 765 770

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2467
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775 780 785

gaa ttg gat ttg ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac
2515
Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr
790 795 800 805

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 Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp
 825 830 835

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 Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr
 840 845 850

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 2707
 Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile
 855 860 865

gtg aag cgt ttc tcc act ggt gcg atg tct tat ggc tcg att tct gct
 2755
 Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala
 870 875 880 885

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 890 895 900

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 2851
 Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu
 905 910 915

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 2899
 Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly
 920 925 930

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 2947
 Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln
 935 940 945

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 950 955 960 965

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 Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro
 970 975 980

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 Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile
 985 990 995

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 Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg
 1000 1005 1010

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 3187
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 1015 1020 1025

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 3235
 Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly
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cac gat ggc gga act ggc gca tct cct ttg acc tcc ctg aag cat gcc
 3283
 His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala
 1050 1055 1060

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 3331
 Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu
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 1095 1100 1105

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 3571
 Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn
 1145 1150 1155

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 1160 1165 1170

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 1175 1180 1185

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3763
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp
          1210          1215          1220

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3811
Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp
          1225          1230          1235

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Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile Thr Arg Ala Ala Ala
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3907
Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser Ile Ser Asn Val Asn
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3955
Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val Ser Arg Val Ala Gly
1270          1275          1280          1285

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4003
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          1290          1295          1300

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4051
Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg Gly Ile Thr Ile Asn
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4099
Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys Gly Leu Ser Gly Gly
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4147
Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn
          1335          1340          1345

aat cca aat atc att gcc gga aac gtg ctt gga tac ggc gca acc agt
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Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly Tyr Gly Ala Thr Ser
1350          1355          1360          1365

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4243
Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg
          1370          1375          1380

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 4339
 Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu
 1400 1405 1410
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 4387
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 1415 1420 1425
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 Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro
 1430 1435 1440 1445
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 4483
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 Ser
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 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
 225 230 235 240
 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
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 Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
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 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
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 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His
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 Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu
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 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu
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Glu	Ala	Ile	Gly	Ser	Met	Gly	Ser	Asp	Thr	Pro	Ile	Ala	Ala	Leu	Ser
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 Met Ser Lys Met Gly Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln
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 945 950 955 960
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 Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys
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113

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Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu	
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Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu	
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Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala	
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Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile	
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Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu	
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 Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
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 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
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 Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
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 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
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Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr
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Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly	
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Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His	
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 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly
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 atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc
 1359
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe
 415 420 425 430
 atc
 1362
 ile

<210> 76

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu Gly Gly
 1 5 10 15

Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu
 20 25 30
 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile
 35 40 45
 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly
 50 55 60
 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser
 65 70 75 80
 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr
 85 90 95
 Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu
 100 105 110
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly
 115 120 125
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys
 130 135 140
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser
 145 150 155 160
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly
 165 170 175
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro
 180 185 190
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser
 195 200 205
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu
 210 215 220
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys
 225 230 235 240
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys
 245 250 255
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly
 260 265 270
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu
 275 280 285
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp
 290 295 300
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val
 305 310 315 320
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala
 325 330 335

Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp
 340 345 350

Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys
 355 360 365

Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala
 370 375 380

Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp
 385 390 395 400

Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile
 420 425 430

<210> 77
 <211> 866
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(843)
 <223> FRXA00367

<400> 77
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 His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
 1 5 10 15

gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att 96
 Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
 20 25 30

gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt 144
 Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
 35 40 45

tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc 192
 Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr
 50 55 60

atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc 240
 Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
 65 70 75 80

atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt 288
 Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
 85 90 95

gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct 336
 Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
 100 105 110

cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac 384
 Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
 115 120 125

gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag 432
 Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
 130 135 140

gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt 480
 Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
 145 150 155 160

gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc 528
 Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
 165 170 175

ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt 576
 Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
 180 185 190

ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat 624
 Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
 195 200 205

ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg 672
 Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
 210 215 220

gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc 720
 Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
 225 230 235 240

aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa 768
 Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
 245 250 255

aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca 816
 Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
 260 265 270

gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga 863
 Ala Ile Lys Ile Met Glu Ala Val Ser
 275 280

ttc 866

<210> 78

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 78

His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
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Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
 20 25 30

Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
 35 40 45

Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr
 50 55 60

Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
 65 70 75 80
 Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
 85 90 95
 Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
 100 105 110
 Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
 115 120 125
 Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
 130 135 140
 Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
 145 150 155 160
 Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
 165 170 175
 Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
 180 185 190
 Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
 195 200 205
 Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
 210 215 220
 Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
 225 230 235 240
 Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
 245 250 255
 Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
 260 265 270
 Ala Ile Lys Ile Met Glu Ala Val Ser
 275 280

<210> 79
 <211> 1494
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1471)
 <223> RXN00076

<400> 79
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 Met Thr Thr Pro Leu
 1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac	163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp	
10 15 20	
ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag	211
Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu	
25 30 35	
caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac	259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp	
40 45 50	
cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac	307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp	
55 60 65	
aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc	355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile	
70 75 80 85	
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc	403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr	
90 95 100	
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa	451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu	
105 110 115	
ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca	499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro	
120 125 130	
cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883

Cys	Gln	Ile	Leu	Glu	Gln	Tyr	Ala	Ile	Arg	Glu	Pro	Lys	Asp	Ala	Pro		
				250					255					260			
cac	acc	ctg	cag	atc	cac	ctc	ttt	gaa	aac	cca	gtt	gag	gtt	ctt	caa	931	
His	Thr	Leu	Gln	Ile	His	Leu	Phe	Glu	Asn	Pro	Val	Glu	Val	Leu	Gln		
			265					270					275				
aag	gac	ggc	aag	gtt	gtt	ggc	ctg	cgc	acc	gaa	cgc	acc	tca	ctt	gat	979	
Lys	Asp	Gly	Lys	Val	Val	Gly	Leu	Arg	Thr	Glu	Arg	Thr	Ser	Leu	Asp		
		280					285					290					
ggc	aac	ggc	ggc	gta	aac	gga	acc	ggc	gaa	ttc	aag	gac	tgg	cca	gtc		
1027																	
Gly	Asn	Gly	Gly	Val	Asn	Gly	Thr	Gly	Glu	Phe	Lys	Asp	Trp	Pro	Val		
	295					300					305						
cag	gct	gtc	tac	cgc	gca	gtc	ggc	tac	aag	tcc	gac	ccc	atc	gac	ggc		
1075																	
Gln	Ala	Val	Tyr	Arg	Ala	Val	Gly	Tyr	Lys	Ser	Asp	Pro	Ile	Asp	Gly		
310					315					320					325		
gtc	cca	ttc	gat	gag	aac	aag	cac	gtc	atc	cct	aat	gac	ggc	gga	cat		
1123																	
Val	Pro	Phe	Asp	Glu	Asn	Lys	His	Val	Ile	Pro	Asn	Asp	Gly	Gly	His		
				330					335					340			
gtc	ctc	acc	gct	cca	ggc	gca	gaa	cca	gta	cca	ggc	ctc	tat	gca	acc		
1171																	
Val	Leu	Thr	Ala	Pro	Gly	Ala	Glu	Pro	Val	Pro	Gly	Leu	Tyr	Ala	Thr		
			345					350					355				
ggc	tgg	atc	aag	cgt	gga	cca	atc	ggt	cta	atc	ggc	aac	acc	aag	tcc		
1219																	
Gly	Trp	Ile	Lys	Arg	Gly	Pro	Ile	Gly	Leu	Ile	Gly	Asn	Thr	Lys	Ser		
		360					365					370					
gac	gcc	aag	gaa	acc	acc	gac	atc	ctc	atc	aag	gat	gcc	gtc	gcc	ggt		
1267																	
Asp	Ala	Lys	Glu	Thr	Thr	Asp	Ile	Leu	Ile	Lys	Asp	Ala	Val	Ala	Gly		
	375					380					385						
gta	ctt	gaa	gct	cca	aag	cac	cag	ggc	gaa	gaa	gcc	atc	atc	gag	ctt		
1315																	
Val	Leu	Glu	Ala	Pro	Lys	His	Gln	Gly	Glu	Glu	Ala	Ile	Ile	Glu	Leu		
390					395					400					405		
ctc	gat	tcc	cgc	aac	atc	cca	ttc	acc	acc	tgg	gaa	ggc	tgg	tac	aaa		
1363																	
Leu	Asp	Ser	Arg	Asn	Ile	Pro	Phe	Thr	Thr	Trp	Glu	Gly	Trp	Tyr	Lys		
				410					415					420			
ctc	gac	gca	gca	gag	cgc	gca	ctc	ggt	gaa	gcc	gaa	ggc	cgc	gag	cgc		
1411																	
Leu	Asp	Ala	Ala	Glu	Arg	Ala	Leu	Gly	Glu	Ala	Glu	Gly	Arg	Glu	Arg		
			425					430					435				
aag	aag	att	gtt	gat	tgg	gaa	gaa	atg	gtc	cgc	cag	gcc	cgc	gaa	gct		
1459																	
Lys	Lys	Ile	Val	Asp	Trp	Glu	Glu	Met	Val	Arg	Gln	Ala	Arg	Glu	Ala		
		440					445					450					

cca gca att gtc taaattgttt taacgcgtga agc

1494

Pro Ala Ile Val

455

<210> 80

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly
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Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe
20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val
180 185 190

Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu
195 200 205

Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu
210 215 220

Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys
225 230 235 240

Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu
245 250 255

Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro

Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
 25 30 35
 caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259
 Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
 40 45 50
 cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307
 His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
 55 60 65
 aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc 355
 Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile
 70 75 80 85
 acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc 403
 Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr
 90 95 100
 ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa 451
 Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu
 105 110 115
 ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca 499
 Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro
 120 125 130
 cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc 547
 Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
 135 140 145
 ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca 595
 Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
 150 155 160 165
 ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643
 Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
 170 175 180
 ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg 691
 Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp
 185 190 195
 ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca 739
 Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro
 200 205 210
 ctc ccc cac cat caa cgt ggt tgt tgatccagaa gacatcgact acg 786
 Leu Pro His His Gln Arg Gly Cys
 215 220

<210> 82

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly
 1 5 10 15



Ile	Tyr	Ala	Ser	Asp	Leu	Leu	Ile	Arg	Asn	Glu	Glu	Arg	Glu	Val	Phe	
			20				25						30			
Val	Asp	Leu	Phe	Glu	Gln	Met	Pro	Ala	Pro	Phe	Gly	Leu	Ile	Arg	Tyr	
			35				40						45			
Gly	Val	Ala	Pro	Asp	His	Pro	Arg	Ile	Lys	Gly	Ile	Val	Lys	Ser	Leu	
			50				55						60			
His	Asn	Val	Leu	Asp	Lys	Pro	Arg	Leu	Arg	Leu	Leu	Gly	Asn	Ile	Glu	
			65				70						75			
Ile	Gly	Lys	Asp	Ile	Thr	Val	Glu	Glu	Leu	Arg	Asp	Tyr	Tyr	Asp	Ala	
			85						90						95	
Val	Val	Phe	Ser	Thr	Gly	Ala	Val	Ala	Asp	Arg	Asp	Leu	Asn	Ile	Pro	
			100						105						110	
Gly	Ile	Glu	Ala	Glu	Gly	Ser	Phe	Gly	Ala	Gly	Glu	Phe	Val	Gly	Phe	
			115						120						125	
Tyr	Asp	Gly	Asn	Pro	Arg	Phe	Glu	Arg	Ser	Trp	Asp	Leu	Ser	Ala	Gln	
			130			135						140				
Ser	Val	Ala	Val	Ile	Gly	Val	Gly	Asn	Val	Gly	Leu	Asp	Val	Ala	Arg	
145						150						155			160	
Ile	Leu	Ala	Lys	Thr	Gly	Asp	Glu	Leu	Lys	Val	Thr	Glu	Ile	Ser	Asp	
			165						170						175	
Asn	Val	Tyr	Asp	Ser	Leu	Lys	Glu	Asn	Lys	Xaa	Xaa	Glu	Val	His	Val	
			180						185						190	
Phe	Gly	Arg	Arg	Trp	Pro	Ser	Thr	Gly	Gln	Val	His	Pro	Thr	Gly	Thr	
			195						200						205	
Xaa	Arg	Thr	Xaa	Pro	Leu	Pro	His	His	Gln	Arg	Gly	Cys				
210						215						220				

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<210> 83
<211> 672
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (649)  
<223> RXN00198
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<400> 83
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ccgcgctcct ttccagcgcg ccgattccac tccatggccg  atg tac ccc aac ctc      115
                                                Met Tyr Pro Asn Leu
                                                1              5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc      163
Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
              10              15              20

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gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211
Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala
25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259
Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu
40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307
Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile
55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355
Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro
70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403
Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu
90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451
Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly
105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499
Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val
120 125 130

tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca 547
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala
135 140 145

atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg 595
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met
150 155 160 165

ggt gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg 643
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu
170 175 180

gct gtc tagcttggt agaaaatgct aga 672
Ala Val

<210> 84

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu
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Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly
20 25 30

Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala
35 40 45

Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu

50 55 60
 Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu
 65 70 75 80
 Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly
 85 90 95
 Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly
 100 105 110
 Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro
 115 120 125
 Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser
 130 135 140
 Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile
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 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
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 gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc 144
 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
 35 40 45
 gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc 192
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60
 cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca 240
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
 65 70 75 80
 ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc 282
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<213> Corynebacterium glutamicum

<400> 86

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 35 40 45

Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(727)

<223> RXN00365

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 Met Ile Leu Ser Pro
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
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tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65

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Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp
70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
150 155 160 165

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Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
185 190 195

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<213> Corynebacterium glutamicum

<400> 88

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35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
85 90 95

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Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
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 Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125
 Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140
 Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160
 Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
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 Ser

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 Met Ile Leu Ser Pro
 1 5
 tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
 10 15 20
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 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35
 gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50
 cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65
 ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp

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Ile Asp Arg Arg	Ile Glu Gln Met Glu	Ala Glu Gly Thr Thr Phe Gln		
	90	95	100	
gta ggc acc tcg ccg cgc gcc gct gaa	cta gcg ctt ttc gac gcg atc	451		
Val Gly Thr Ser Pro Arg Ala Ala Glu	Leu Ala Leu Phe Asp Ala Ile			
	105	110	115	
ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc	tca gtt cca ggc	499		
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu	Ser Val Pro Gly			
	120	125	130	
cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa	547			
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln				
	135	140	145	
aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa	595			
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys				
	150	155	160	165
ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc	643			
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys				
	170	175	180	
ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat	691			
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp				
	185	190	195	
atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc	727			
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser				
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Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala				
	35	40	45	
Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg				
	50	55	60	
Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys				
	65	70	75	80
Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu				
	85	90	95	
Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala				
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Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125
 Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140
 Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160
 Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175
 Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
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 Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
 195 200 205
 Ser

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 Met Ala Asp Pro Gln
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 gga ttc atc aaa tac tcc cga cgc gag cct gca cac cgc ccg gtc ccg 163
 Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro
 10 15 20
 ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt 211
 Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly
 25 30 35
 cag atc gag gaa cag gct gcc cgc tgc atg gat tgc ggt gtc ccg ttc 259
 Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe
 40 45 50
 tgc cac gaa ggc tgc cca ctg ggc aac atc atc cct gag tgg aat gat 307
 Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp
 55 60 65
 ctg gta cgc caa ggt cgg tgg aag gaa gcc tac gat cgc ttg cac gcg 355
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                                         Met Thr Val Asp Glu
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cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163

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Pro	Glu	Phe	His	Gln	Ala	Val	Ala	Glu	Val	Leu	Glu	Ser	Leu	Lys	Ile		
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gtc	ctg	gaa	aag	gac	cct	cat	tac	gct	gat	tac	ggg	ctc	atc	cag	cgc	259	
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Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg	Phe	His	Pro	Ser	Val		
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Asn	Leu	Gly	Ile	Val	Lys	Phe	Leu	Gly	Phe	Glu	Gln	Ile	Phe	Lys	Asn		
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His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser	Gly	Val	Leu	Thr	Gly		
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Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile	Lys	Ala	Lys	Gly	Glu		
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Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly	Ser	Gly	Asn	Val	Ala		
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Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	Ala	Thr	Val	Ile	Gly		

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Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	Ala	Arg	Val	Ser	Val					
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1027																				
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1267																				
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		375				380						385								
gat	tcc	tgg	agc	ttc	gag	tac	acc	gac	gag	cgc	ctc	cag	gtg	atc	atg					
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390					395					400					405					
aag	aac	atc	ttc	aag	acc	tgt	gca	gag	acc	gca	gca	gag	tat	gga	cac					
1363																				
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1411																				
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1464

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Glu	Ser	Leu	Lys	Ile	Val	Leu	Glu	Lys	Asp	Pro	His	Tyr	Ala	Asp	Tyr
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Gly	Leu	Ile	Gln	Arg	Leu	Cys	Glu	Pro	Glu	Arg	Gln	Leu	Ile	Phe	Arg
	50					55					60				
Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe
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Arg	Val	Gln	Phe	Asn	Ser	Ala	Leu	Gly	Pro	Tyr	Lys	Gly	Gly	Leu	Arg
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Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met
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Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asn	Ile	Gly	Val	Gly	Gly	His	Glu	Ile
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Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly
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Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly
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Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro
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 Ala Arg Val Ser Val Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His
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 Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
 305 310 315 320
 Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
 325 330 335
 Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
 340 345 350
 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
 355 360 365
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380
 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 385 390 395 400
 Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
 405 410 415
 Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430
 Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
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 <213> Corynebacterium glutamicum

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 Met Asn Ser Glu Gln
 1 5
 gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt 163
 Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg
 10 15 20
 cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct 211
 Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala
 25 30 35
 cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc 259
 Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly

40	45	50	
tca gcc att gag ggc tac gcg cgt atc tcg gaa gcg gac acc att gcc			307
Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu Ala Asp Thr Ile Ala			
55	60	65	
cgc cca gat cca tcg aca ttc cag gtc ctc cca cta gaa gcg ggc atc			355
Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro Leu Glu Ala Gly Ile			
70	75	80	85
tca aaa ctg cag gca gca cgc ctg ttt tgc gat gtc acg atg cca gac			403
Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp Val Thr Met Pro Asp			
	90	95	100
gga cag cca tct ttt tct gac ccg cgc caa gtg ctg cgc agg cag gtc			451
Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val Leu Arg Arg Gln Val			
	105	110	115
caa cta gct gca gat gaa ggc ttg acc tgc atg atc tca cca gag att			499
Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met Ile Ser Pro Glu Ile			
	120	125	130
gag ttc tat ttg gtg caa agc ctt cgc acc aac gga ctg cca cct gtg			547
Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn Gly Leu Pro Pro Val			
	135	140	145
ccc act gac aac ggc gga tat ttc gac caa gcc aca ttc aat gag gcg			595
Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala Thr Phe Asn Glu Ala			
150	155	160	165
ccg aat ttc cgt cga aac gcg atg gta gcg ctg gag gaa ctc ggc atc			643
Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu Glu Glu Leu Gly Ile			
	170	175	180
cct gtc gag ttc tcc cac cat gaa act gca cct ggc cag caa gaa atc			691
Pro Val Glu Phe Ser His His Glu Thr Ala Pro Gly Gln Gln Glu Ile			
	185	190	195
gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc			739
Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr			
	200	205	210
ttc cgc tac atc atg aaa cag gtg gca agg gac caa ggc gtc ggg gca			787
Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp Gln Gly Val Gly Ala			
	215	220	225
tca ttt atg ccc aag cca ttc caa gaa cat gca ggc tcc gcc atg cac			835
Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala Gly Ser Ala Met His			
230	235	240	245
acg cac atg tcc tta ttt gag ggc gat acc aac gcg ttc cac gat cca			883
Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn Ala Phe His Asp Pro			
	250	255	260
gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga			931
Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly			
	265	270	275
atc ttg cat cac gct cca gaa ttc acc gct gtg acc aac cag tgg gtc			979
Ile Leu His His Ala Pro Glu Phe Thr Ala Val Thr Asn Gln Trp Val			
	280	285	290

aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca
1027

Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala
295 300 305

acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac
1075

Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr
310 315 320 325

cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat
1123

Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp
330 335 340

acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt
1171

Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly
345 350 355

ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac
1219

Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp
360 365 370

gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac
1267

Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn
375 380 385

gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca
1315

Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser
390 395 400 405

gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg
1363

Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu
410 415 420

cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg
1411

Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro
425 430 435

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1458

Trp Glu Leu Arg Asn Asn Leu Asp Tyr
440 445

gaa
1461

<210> 96

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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 Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly
 35 40 45
 Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu
 50 55 60
 Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
 65 70 75 80
 Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp
 85 90 95
 Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val
 100 105 110
 Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met
 115 120 125
 Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn
 130 135 140
 Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala
 145 150 155 160
 Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu
 165 170 175
 Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro
 180 185 190
 Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala
 195 200 205
 Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp
 210 215 220
 Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala
 225 230 235 240
 Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn
 245 250 255
 Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys
 260 265 270
 Gln Phe Ile Ala Gly Ile Leu His His Ala Pro Glu Phe Thr Ala Val
 275 280 285
 Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu
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<211> 1554
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (1531)
<223> RXA00335
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ccg gaa gaa att gtc aag ttc atc aag gat gaa aac gtc gag ttc gtt															163	
Pro	Glu	Glu	Ile	Val	Lys	Phe	Ile	Lys	Asp	Glu	Asn	Val	Glu	Phe	Val	
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gac gtt cga ttc acc gac ctt ccc ggc acc gag cag cac ttc agc atc															211	
Asp	Val	Arg	Phe	Thr	Asp	Leu	Pro	Gly	Thr	Glu	Gln	His	Phe	Ser	Ile	
			25					30					35			
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Pro	Ala	Ala	Ser	Phe	Asp	Ala	Asp	Thr	Ile	Glu	Glu	Gly	Leu	Ala	Phe	
		40					45					50				
gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg															307	
Asp	Gly	Ser	Ser	Ile	Arg	Gly	Phe	Thr	Thr	Ile	Asp	Glu	Ser	Asp	Met	
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aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag															355	
Asn	Leu	Leu	Pro	Asp	Leu	Gly	Thr	Ala	Thr	Leu	Asp	Pro	Phe	Arg	Lys	
70					75					80					85	

gca aag acc ctg aac gtt aag ttc ttc gtt cac gat cct ttc acc cgc	403
Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg	
90 95 100	
gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag	451
Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln	
105 110 115	
tac ctg gca tcc acc ggc att gca gac acc tgc aac ttc ggc gcc gag	499
Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu	
120 125 130	
gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac	547
Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn	
135 140 145	
tcc ggc ttc tac gaa gta gat acc gaa gaa ggc tgg tgg aac cgt ggc	595
Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly	
150 155 160 165	
aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc	643
Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg	
170 175 180	
gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac	691
Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp	
185 190 195	
gtg cgc gat gac atg gtt cgc aac ctc gca gct tcc ggc ttc gct ctt	739
Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu	
200 205 210	
gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac	787
Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr	
215 220 225	
cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag	835
Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys	
230 235 240 245	
tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc	883
Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe	
250 255 260	
atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac	931
Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His	
265 270 275	
cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc	979
Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe His Asp Glu Ser Gly	
280 285 290	
tac gca ggc ctg tcc gac atc gcc cgc tac tac atc ggc ggc atc ctg	
1027	
Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr Ile Gly Gly Ile Leu	
295 300 305	
cac cac gca ggc gct gtt ctg gcg ttc acc aac gca acc ctg aac tcc	
1075	
His His Ala Gly Ala Val Leu Ala Phe Thr Asn Ala Thr Leu Asn Ser	
310 315 320 325	

tac cac cgt ctg gtt cca ggc ttc gag gct cca atc aac ctg gtg tac
 1123
 Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro Ile Asn Leu Val Tyr
 330 335 340

tca cag cgc aac cgt tcc gct gct gtc cgt atc cca atc acc gga tcc
 1171
 Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile Pro Ile Thr Gly Ser
 345 350 355

aac ccg aag gca aag cgc atc gaa ttc cgc gct cca gac cca tca ggc
 1219
 Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala Pro Asp Pro Ser Gly
 360 365 370

aac cca tac ctg ggc ttt gca gcg atg atg atg gcc ggc ctc gac ggc
 1267
 Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met Ala Gly Leu Asp Gly
 375 380 385

atc aag aac cgc atc gag cca cac gct cca gtg gac aag gac ctc tac
 1315
 Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val Asp Lys Asp Leu Tyr
 390 395 400 405

gaa cta cca cca gag gaa gct gca tcc att cca cag gca cca acc tcc
 1363
 Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro Gln Ala Pro Thr Ser
 410 415 420

ctg gaa gca tcc ctg aag gca ctg cag gaa gac acc gac ttc ctc acc
 1411
 Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp Thr Asp Phe Leu Thr
 425 430 435

gag tct gac gtc ttc acc gag gat ctc atc gag gcg tac atc cag tac
 1459
 Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu Ala Tyr Ile Gln Tyr
 440 445 450

aag tac gac aac gag atc tcc cca gtt cgc ctg cgc cca acc ccg cag
 1507
 Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu Arg Pro Thr Pro Gln
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 470 475

<210> 98

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

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 35 40 45
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
 50 55 60
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
 65 70 75 80
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
 85 90 95
 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
 100 105 110
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
 115 120 125
 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
 130 135 140
 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
 145 150 155 160
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
 165 170 175
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
 180 185 190
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
 195 200 205
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
 210 215 220
 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
 225 230 235 240
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
 245 250 255
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
 260 265 270
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
 275 280 285
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
 290 295 300
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
 305 310 315 320
 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
 325 330 335
 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

340	345	350
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355	360	365
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met		
370	375	380
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val		
385	390	395
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro		
405	410	415
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp		
420	425	430
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu		
435	440	445
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu		
450	455	460
Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys		
465	470	475

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 <211> 3258
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(3235)
 <223> RXA00324

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 Met Ser Gly Pro Leu
 1 5
 aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa 163
 Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys
 10 15 20
 gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag 211
 Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu
 25 30 35
 cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg 259
 His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu
 40 45 50
 tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg 307
 Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu
 55 60 65
 tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat 355

Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala	Arg	Asn	Glu	Leu	Asp	
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Gln	Glu	Ile	Arg	Gln	Asp	Glu	Lys	Leu	Arg	Val	Arg	Leu	Phe	Ala	Leu	
				90					95					100		
ttg	ggt	ggt	tcc	tcg	gct	gtc	ggt	gat	cac	ttg	gtc	gcc	aat	cct	ttg	451
Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	Val	Ala	Asn	Pro	Leu	
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cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	agg	gaa	gag	atg	ttt	499
Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	Arg	Glu	Glu	Met	Phe	
		120					125					130				
cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	gct	gtg	ctt	gag	gtt	547
Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	Ala	Val	Leu	Glu	Val	
	135					140					145					
gag	gat	ttc	agc	gat	gca	cac	aac	att	gcc	cga	gac	gat	ttg	agc	acg	595
Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	Asp	Asp	Leu	Ser	Thr	
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Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro	Glu	Ala	Glu	Arg	Val	
				170					175					180		
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Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	Ile	Ala	Ala	His	Asp	
			185					190					195			
tta	gcg	ggt	acc	tat	ccc	acc	gac	atg	cgg	aga	aaa	ggt	ggc	gat	cct	739
Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	Lys	Gly	Gly	Asp	Pro	
		200					205					210				
gtt	ccg	ttt	agc	aca	gtg	acc	atg	cag	ctc	agc	gac	cta	gct	gat	gct	787
Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	Asp	Leu	Ala	Asp	Ala	
	215					220					225					
gct	ttg	act	gct	gct	tta	gct	gtg	gca	att	gcc	aat	gtt	tat	ggt	gaa	835
Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	Asn	Val	Tyr	Gly	Glu	
230					235				240						245	
aag	ccg	gtt	gat	tca	gct	tta	tct	gtc	atc	gcg	atg	ggc	aaa	tgt	ggc	883
Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	Met	Gly	Lys	Cys	Gly	
				250					255					260		
gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	gtg	gtg	ttt	gtt	gca	931
Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	Val	Val	Phe	Val	Ala	
			265					270					275			
gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979
Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	Ala	Glu	Leu	Ile	Arg	
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1027																
Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	Ala	Leu	Arg	Pro	Glu	
	295					300					305					

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 1075
 Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr
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 1123
 Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala
 330 335 340
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 1171
 Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala
 345 350 355
 ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca
 1219
 Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr
 360 365 370
 gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac
 1267
 Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp
 375 380 385
 ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg
 1315
 Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val
 390 395 400 405
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 1363
 Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu
 410 415 420
 acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat
 1411
 Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp
 425 430 435
 cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat
 1459
 Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr
 440 445 450
 gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag
 1507
 Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys
 455 460 465
 cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg
 1555
 Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp
 470 475 480 485
 ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc
 1603
 Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala
 490 495 500

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg
 1651
 Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser
 505 510 515

ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac
 1699
 Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn
 520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa
 1747
 Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln
 535 540 545

ttg gcg gca ttg gga tac ctg cat cca tca cgt gct tat gaa cac ctg
 1795
 Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu
 550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg
 1843
 Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met
 570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat
 1891
 Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp
 585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc
 1939
 Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg
 600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg
 1987
 Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg
 615 620 625

ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc
 2035
 Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile
 630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct
 2083
 Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro
 650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca
 2131
 Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala
 665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga
 2179
 Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg
 680 685 690

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc
 2227
 Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu
 695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg
 2275
 Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp
 710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt
 2323
 Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu
 730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc
 2371
 Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile
 745 750 755

ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc
 2419
 Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala
 760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag
 2467
 Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu
 775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt
 2515
 Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu
 790 795 800 805

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt
 2563
 Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg
 810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg
 2611
 Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val
 825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg
 2659
 Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu
 840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg
 2707
 Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu
 855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg
 2755
 Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala
 870 875 880 885

cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg
 2803
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg
 890 895 900

ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga
 2851
 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly
 905 910 915

gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat
 2899
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His
 920 925 930

gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt
 2947
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu
 935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg
 2995
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr
 950 955 960 965

ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg
 3043
 Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val
 970 975 980

ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac
 3091
 Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His
 985 990 995

ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag
 3139
 Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln
 1000 1005 1010

gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt
 3187
 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val
 1015 1020 1025

gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt
 3235
 Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe
 1030 1035 1040 1045

taggtagggtg gtgggagccc caa
 3258

<210> 100

<211> 1045

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg

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Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	35	40	45
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val	85	90	95
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
 340 345 350
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
 355 360 365
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
 420 425 430
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
 435 440 445
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
 450 455 460
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
 485 490 495
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
 500 505 510
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
 545 550 555 560
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
 565 570 575
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
 580 585 590
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
 595 600 605
 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
 610 615 620
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
 625 630 635 640
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp
 645 650 655

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
 660 665 670
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
 675 680 685
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
 690 695 700
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
 705 710 715 720
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu
 725 730 735
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
 740 745 750
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
 755 760 765
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
 770 775 780
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser
 785 790 795 800
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val
 805 810 815
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr
 820 825 830
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu
 835 840 845
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
 850 855 860
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp
 865 870 875 880
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg
 885 890 895
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr
 900 905 910
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu
 915 920 925
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser
 930 935 940
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro
 945 950 955 960
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala
 965 970 975
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro

980 985 990
 Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp
 995 1000 1005
 Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg
 1010 1015 1020
 Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met
 1025 1030 1035 1040
 Glu Gln Arg Glu Phe
 1045

<210> 101
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(861)
 <223> RXN03176

<400> 101
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 ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30
 gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45
 tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc 192
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60
 gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac 240
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80
 ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc 288
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95
 atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg 336
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc 384
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac 432
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160

 gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175

 acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190

 aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205

 ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220

 cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240

 gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255

 cca cgc ctg aac ccc aaa ggc aac agc gtg cgc gcc gta aaa ata ttc 816
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270

 aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 102

<211> 287

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 102

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 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80

 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255
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 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 103
 <211> 861
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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(861)
 <223> FRXA02879

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 ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30
 gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
260 265 270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag	861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu	
275 280 285	

<210> 104
 <211> 287
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 104
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 20 25 30
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

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<211> 1155
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1132)  
<223> RXA00278
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gtgggtcggc atccgcccc gtttgcagga gtacttataa atg cac gct ttt cga															115	
Met His Ala Phe Arg															5	
1																
cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca	10					15					20					163
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala																
acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc	25					30					35					211
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr																
ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct	40					45					50					259
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser																
tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag	55					60					65					307
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu																
aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg	70					75					80					355
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg																85
gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa	90					95					100					403
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln																
tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc	105					110					115					451
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg																
ggt ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt	120					125					130					499
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly																
gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg	135					140					145					547
Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu																
cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg	150					155					160					595
Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr																165
atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg	170					175					180					643
Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu																

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser
 185 190 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
 200 205 210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
 215 220 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
 230 235 240 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
 250 255 260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
 265 270 275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979
 Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu
 280 285 290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg
 1027
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met
 295 300 305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac
 1075
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
 310 315 320 325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac
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 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn
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 Asp Glu Gly

<210> 106

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val
 20 25 30

Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro
 35 40 45
 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile
 50 55 60
 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu
 65 70 75 80
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile
 85 90 95
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val
 100 105 110
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser
 115 120 125
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly
 130 135 140
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val
 145 150 155 160
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe
 165 170 175
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser
 180 185 190
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val
 195 200 205
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu
 210 215 220
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu
 225 230 235 240
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser
 245 250 255
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu
 260 265 270
 Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr
 275 280 285
 Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile
 290 295 300
 Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro
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 Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu
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 Glu Gly Thr Glu Asn Asp Glu Gly
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<211> 1035
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<213> Corynebacterium glutamicum
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				Leu	Arg	Phe	Pro	Lys									
				1				5									
atc	ccc	aag	cgc	gct	gta	gcg	gcg	acc	gtc	ggc	atc	gtg	gca	acc	tca	163	
Ile	Pro	Lys	Arg	Ala	Val	Ala	Ala	Thr	Val	Gly	Ile	Val	Ala	Thr	Ser		
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ttc	acc	ttg	gct	tct	tgt	gtc	acc	aat	gag	gag	cag	ggc	aac	cca	gat	211	
Phe	Thr	Leu	Ala	Ser	Cys	Val	Thr	Asn	Glu	Glu	Gln	Gly	Asn	Pro	Asp		
			25					30					35				
ggc	tgg	gag	cag	atc	gtt	cca	gat	cct	gta	ccg	gag	att	cag	gcg	atg	259	
Gly	Trp	Glu	Gln	Ile	Val	Pro	Asp	Pro	Val	Pro	Glu	Ile	Gln	Ala	Met		
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gtt	ccc	gaa	gct	ctg	gct	cag	cgc	ggt	gtg	ctc	acc	gcc	ggg	gcc	aac	307	
Val	Pro	Glu	Ala	Leu	Ala	Gln	Arg	Gly	Val	Leu	Thr	Ala	Gly	Ala	Asn		
	55					60					65						
cca	cct	ttc	cca	ccg	ttt	gag	ttt	aaa	gat	tcc	gat	ggg	cag	att	atc	355	
Pro	Pro	Phe	Pro	Pro	Phe	Glu	Phe	Lys	Asp	Ser	Asp	Gly	Gln	Ile	Ile		
70					75					80					85		
ggg	gtg	gaa	atg	gac	ctc	gtg	cgt	gca	atg	gcg	ggg	gtg	atg	ggc	ttg	403	
Gly	Val	Glu	Met	Asp	Leu	Val	Arg	Ala	Met	Ala	Gly	Val	Met	Gly	Leu		
			90					95						100			
gag	ttc	agc	cct	cag	gag	cag	gat	ttc	tcc	ctc	atc	ctt	cca	tcg	gtt	451	
Glu	Phe	Ser	Pro	Gln	Glu	Gln	Asp	Phe	Ser	Leu	Ile	Leu	Pro	Ser	Val		
			105					110					115				
caa	gct	ggc	acc	ctt	gat	atc	gga	gcc	tct	ggc	ttc	act	gac	aac	gag	499	
Gln	Ala	Gly	Thr	Leu	Asp	Ile	Gly	Ala	Ser	Gly	Phe	Thr	Asp	Asn	Glu		
		120					125					130					
gaa	cgc	cgc	gag	aac	ttt	gat	ttc	atc	gat	ttc	ctc	ttc	gca	ggg	gtg	547	
Glu	Arg	Arg	Glu	Asn	Phe	Asp	Phe	Ile	Asp	Phe	Leu	Phe	Ala	Gly	Val		
	135					140					145						
cag	tgg	gcg	cag	gca	act	gat	cgt	gaa	acc	cca	atc	gat	ccg	gaa	aac	595	
Gln	Trp	Ala	Gln	Ala	Thr	Asp	Arg	Glu	Thr	Pro	Ile	Asp	Pro	Glu	Asn		
150					155					160					165		
gcc	tgt	ggg	ctc	acc	gtt	gct	gta	cag	cgc	aca	acc	gtg	gca	gag	acc	643	
Ala	Cys	Gly	Leu	Thr	Val	Ala	Val	Gln	Arg	Thr	Thr	Val	Ala	Glu	Thr		
			170					175					180				

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu
 185 190 195

 ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
 200 205 210

 ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
 215 220 225

 gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
 230 235 240 245

 atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
 250 255 260

 ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
 Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
 265 270 275

 gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
 280 285 290

 gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa
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 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
 295 300

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 1035

<210> 108
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
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 Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu
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 Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro
 35 40 45

 Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
 50 55 60

 Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
 65 70 75 80

 Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala
 85 90 95

Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu
 100 105 110
 Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly
 115 120 125
 Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe
 130 135 140
 Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro
 145 150 155 160
 Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr
 165 170 175
 Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu
 180 185 190
 Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp
 195 200 205
 Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala
 210 215 220
 Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile
 225 230 235 240
 Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe
 245 250 255
 Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His
 260 265 270
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 Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
 290 295 300

<210> 109
 <211> 1962
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1939)
 <223> RXA02139

<400> 109
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 Met Arg His Arg Gly
 1 5
 cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

Pro	Asp	Asp	Ala	Gly	Thr	Trp	His	Asp	Ala	Asp	Ala	Ala	Phe	Gly	Phe	
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aac	cgc	ctc	tcc	atc	att	gat	att	gca	cac	tcc	cac	caa	cca	ctg	cgt	211
Asn	Arg	Leu	Ser	Ile	Ile	Asp	Ile	Ala	His	Ser	His	Gln	Pro	Leu	Arg	
			25					30					35			
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Trp	Gly	Pro	Ala	Asp	Glu	Pro	Asp	Arg	Tyr	Ala	Met	Thr	Phe	Asn	Gly	
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Glu	Ile	Tyr	Asn	Tyr	Val	Glu	Leu	Arg	Lys	Glu	Leu	Ser	Asp	Leu	Gly	
	55					60					65					
tat	gcc	ttt	aat	act	tct	ggc	gat	ggc	gag	cca	att	gtt	gtc	ggc	ttc	355
Tyr	Ala	Phe	Asn	Thr	Ser	Gly	Asp	Gly	Glu	Pro	Ile	Val	Val	Gly	Phe	
	70				75					80					85	
cac	cac	tgg	ggc	gag	tcc	gtg	gtc	gag	cat	ctc	cgc	gga	atg	ttc	ggc	403
His	His	Trp	Gly	Glu	Ser	Val	Val	Glu	His	Leu	Arg	Gly	Met	Phe	Gly	
			90						95					100		
att	gcc	att	tgg	gat	aca	aag	gaa	aag	tcg	ctt	ttc	ctt	gcg	cgt	gat	451
Ile	Ala	Ile	Trp	Asp	Thr	Lys	Glu	Lys	Ser	Leu	Phe	Leu	Ala	Arg	Asp	
			105					110						115		
cag	ttc	ggc	att	aag	cca	ctg	ttc	tac	gca	acc	acc	gag	cat	ggc	acc	499
Gln	Phe	Gly	Ile	Lys	Pro	Leu	Phe	Tyr	Ala	Thr	Thr	Glu	His	Gly	Thr	
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gtg	ttc	tcc	tca	gag	aag	aag	acc	atc	ttg	gag	atg	gcc	gag	gag	atg	547
Val	Phe	Ser	Ser	Glu	Lys	Lys	Thr	Ile	Leu	Glu	Met	Ala	Glu	Glu	Met	
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aat	cta	gat	ctg	ggc	ctt	gat	aag	cgc	acc	att	gag	cac	tac	gtg	gac	595
Asn	Leu	Asp	Leu	Gly	Leu	Asp	Lys	Arg	Thr	Ile	Glu	His	Tyr	Val	Asp	
	150				155					160					165	
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Leu	Gln	Tyr	Val	Pro	Glu	Pro	Asp	Thr	Leu	His	Ala	Gln	Ile	Ser	Arg	
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Leu	Glu	Ser	Gly	Cys	Thr	Ala	Thr	Val	Arg	Pro	Gly	Gly	Lys	Leu	Glu	
			185					190					195			
cag	aag	cgt	tac	ttc	aag	cct	cag	ttc	cca	gta	cag	aag	gtc	gta	aag	739
Gln	Lys	Arg	Tyr	Phe	Lys	Pro	Gln	Phe	Pro	Val	Gln	Lys	Val	Val	Lys	
		200					205					210				
ggc	aag	gag	cag	gac	ctc	ttc	gat	cgc	att	gcc	cag	gtg	ttg	gag	gat	787
Gly	Lys	Glu	Gln	Asp	Leu	Phe	Asp	Arg	Ile	Ala	Gln	Val	Leu	Glu	Asp	
	215					220					225					
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Ser	Val	Glu	Lys	His	Met	Arg	Ala	Asp	Val	Thr	Val	Gly	Ser	Phe	Leu	
	230				235				240						245	
ttc	ggc	ggc	att	gac	tca	acc	gca	att	gcg	gcg	ctt	gca	aag	cgc	cac	883
Phe	Gly	Gly	Ile	Asp	Ser	Thr	Ala	Ile	Ala	Ala	Leu	Ala	Lys	Arg	His	

250										255					260						
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Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr																					
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Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu																					
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cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct																					
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His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro																					
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aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc																					
1075																					
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val																					
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ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg																					
1123																					
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val																					
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ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac																					
1171																					
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr																					
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1219																					
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu																					
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cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag																					
1267																					
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys																					
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ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac																					
1315																					
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr																					
390	395										400					405					
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1363																					
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile																					
410										415					420						
cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc																					
1411																					
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile																					
425										430					435						
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg																					
1459																					
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu																					
440										445					450						

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 1507
 Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys
 455 460 465

 atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag
 1555
 Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys
 470 475 480 485

 gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc
 1603
 Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
 490 495 500

 aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt
 1651
 Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
 505 510 515

 ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg
 1699
 Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
 520 525 530

 cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc
 1747
 Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
 535 540 545

 atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg
 1795
 Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
 550 555 560 565

 gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga
 1843
 Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
 570 575 580

 ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa
 1891
 Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
 585 590 595

 aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt
 1939
 Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
 600 605 610

 taagtcttaa agcctaaacc ccc
 1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

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His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala	35	40	45
Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu	50	55	60
Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro	65	70	75
Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu	85	90	95
Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu	100	105	110
Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr	115	120	125
Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu	130	135	140
Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile	145	150	155
Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His	165	170	175
Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro	180	185	190
Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val	195	200	205
Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala	210	215	220
Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr	225	230	235
Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala	245	250	255
Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe	260	265	270
Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala	275	280	285
Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr	290	295	300
Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala	305	310	315
Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys	325	330	335

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly
 340 345 350
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys
 355 360 365
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu
 370 375 380
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr
 385 390 395 400
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln
 405 410 415
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu
 420 425 430
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
 435 440 445
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
 450 455 460
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
 465 470 475 480
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
 485 490 495
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
 500 505 510
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
 515 520 525
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
 530 535 540
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
 545 550 555 560
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
 565 570 575
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
 580 585 590
 Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
 595 600 605
 Tyr Pro Val Glu Leu
 610

<210> 111

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum



<220>
 <221> CDS
 <222> (101)..(1261)
 <223> RXN00116

<400> 111

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cgcggcacgc acgctggggg caagcgctcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
                                         Met Ser Asn Asp Phe
                                         1                               5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
                        10                               15                               20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
                        25                               30                               35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
                        40                               45                               50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
                        55                               60                               65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
                        70                               75                               80                               85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                        90                               95                               100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
                        105                               110                               115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
                        120                               125                               130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
                        135                               140                               145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
                        150                               155                               160                               165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
                        170                               175                               180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
                        185                               190                               195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739

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Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln
    200                                205                                210

aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg      787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
    215                                220                                225

acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg      835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
    230                                235                                240                                245

ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg      883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
    250                                255                                260

aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg      931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
    265                                270                                275

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag      979
Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
    280                                285                                290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg
1027
Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
    295                                300                                305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat
1075
Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
    310                                315                                320                                325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag
1123
Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
    330                                335                                340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
1171
Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
    345                                350                                355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
1219
Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
    360                                365                                370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
1261
Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
    375                                380                                385

tagtttgaac aggttggttg ggg
1284

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<210> 112

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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Met Ser Asn' Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
 1           5           10           15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
      20           25           30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
      35           40           45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50           55           60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65           70           75

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
      85           90           95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
      100           105           110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115           120           125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130           135           140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145           150           155           160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
      165           170           175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
      180           185           190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195           200           205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210           215           220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225           230           235           240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
      245           250           255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
      260           265           270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
      275           280           285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290           295           300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305           310           315           320

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[illegible]

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<210> 113
<211> 607
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> FRXA00116
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<400> 113																
tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atgagtaatg acttcgctcgt																60
ttctaggcctt agaccctttg gtgaaacgat ttttgcaacc																115
Met Thr Gln Arg Ala																
1 5																
gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat																163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp																
10 15 20																
ggc cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga																211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly																
25 30 35																
aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct																259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala																
40 45 50																
gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat																307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp																
55 60 65																
tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act																355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr																
70 75 80 85																
gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg																403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro																
90 95 100																
tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg ccg																451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg																
105 110 115																

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 114
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 114
 Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
 1 5 10 15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val
 85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu
 100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser
 115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr
 130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe
 145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala
 165

<210> 115
 <211> 1230
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1207)

<223> RXN00618

<400> 115

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gctgcattag agggctcgtat ctcgatctaa aagcagtacg cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1                               5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                        15                        20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                        30                        35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                        45                        50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                        60                        65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                        75                        80                        85

ggg gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                        90                        95                        100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105                        110                        115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                        120                        125                        130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135                        140                        145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
                        150                        155                        160                        165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170                        175                        180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                        185                        190                        195

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ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739
Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
      200                      205                      210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
      215                      220                      225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
      230                      235                      240                      245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
      250                      255                      260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
      265                      270                      275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
      280                      285                      290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
1027
Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
      295                      300                      305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
1075
Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
      310                      315                      320                      325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
1123
Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
      330                      335                      340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
      345                      350                      355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
      360                      365

taggttagtt tcg
1230

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<210> 116

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp

1	5	10	15
Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala	20	25	30
Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr	35	40	45
Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp	50	55	60
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val	65	70	75
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu	85	90	95
Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr	100	105	110
Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys	115	120	125
Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu	130	135	140
Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr	145	150	155
Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys	165	170	175
Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met	180	185	190
Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala	195	200	205
Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg	210	215	220
Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn	225	230	235
Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala	245	250	255
Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His	260	265	270
Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro	275	280	285
Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu	290	295	300
Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu	305	310	315
Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe	325	330	335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365

Lys

<210> 117

<211> 657

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcatga 60

caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
 105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
 120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175

taggttagtt tcg 657

<210> 118
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 118
 Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 119
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 119

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gaagccaagc actagaagca atgttcagcc gtttcgcgct atg cag atg ttg gac 115
                                   Met Gln Met Leu Asp
                                   1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                                   10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                                   25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                                   40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                                   55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                                   70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
                                   90 95

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<210> 120
 <211> 95
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 120

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Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
  1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
  20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
  35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
  50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
  65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
  85 90 95

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<210> 121
 <211> 1434
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1411)
 <223> RXA02550

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 tagctttcaa ctacgcacac aaagtggcaa cattgagcgg gtg act aca gac aag 115
 Val Thr Thr Asp Lys
 1 5
 cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163
 Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala
 10 15 20
 gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211
 Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp
 25 30 35
 cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259
 Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val
 40 45 50
 gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307
 Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys
 55 60 65
 ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg 355
 Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val
 70 75 80 85
 att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc 403
 Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser
 90 95 100
 acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac 451
 Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr
 105 110 115
 gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta 499
 Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu
 120 125 130
 ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc 547
 Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu
 135 140 145
 aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg 595
 Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp
 150 155 160 165
 act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt 643
 Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys

170	175	180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa			691
Asp Glu Glu Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys			
185	190	195	
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc			739
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro			
200	205	210	
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att			787
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile			
215	220	225	
gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc			835
Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg			
230	235	240	245
att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca			883
Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro			
250	255	260	
gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc			931
Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val			
265	270	275	
gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac			979
Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr			
280	285	290	
gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc			
1027			
Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu			
295	300	305	
tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga			
1075			
Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly			
310	315	320	325
cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa			
1123			
Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu			
330	335	340	
cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc			
1171			
Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser			
345	350	355	
tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc			
1219			
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro			
360	365	370	
aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc			
1267			
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu			
375	380	385	

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405
 cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420
 gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
 425 430 435
 tagtagttgt taggattcac cac
 1434

<210> 122
 <211> 437
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 122
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 Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr
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 Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
 35 40 45
 Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
 50 55 60
 His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
 65 70 75 80
 Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
 85 90 95
 Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
 100 105 110
 Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
 115 120 125
 Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
 130 135 140
 Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
 145 150 155 160
 Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
 165 170 175
 Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
 180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
 195 200 205
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
 210 215 220
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
 225 230 235 240
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
 245 250 255
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
 260 265 270
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430
 Ser Thr Tyr Lys Gln
 435

<210> 123

<211> 1701

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1678)

<223> RXA02193

<400> 123

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190

aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat 835
 Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp
 230 235 240 245

gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac 883
 Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn
 250 255 260

ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc 931
 Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu
 265 270 275

gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca 979
 Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro
 280 285 290

gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga
 1027
 Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly
 295 300 305

ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc
 1075
 Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr
 310 315 320 325

ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa
 1123
 Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys
 330 335 340

ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt
 1171
 Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg
 345 350 355

gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc
 1219
 Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser
 360 365 370

atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag
 1267
 Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln
 375 380 385

gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg
 1315
 Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala
 390 395 400 405

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa
 1363
 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu
 410 415 420

tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg
 1411
 Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu
 425 430 435

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt
 1459
 Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg
 440 445 450

 gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc
 1507
 Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe
 455 460 465

 ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act
 1555
 Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr
 470 475 480 485

 ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa
 1603
 Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu
 490 495 500

 aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg
 1651
 Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met
 505 510 515

 ttc cgc gga agg ctc tac ttg gag aac taatccaaga tctcgtctga
 1698
 Phe Arg Gly Arg Leu Tyr Leu Glu Asn
 520 525

 tac
 1701

<210> 124
 <211> 526
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 124
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 20 25 30

 Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro
 35 40 45

 Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly
 50 55 60

 Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg
 65 70 75 80

 Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro
 85 90 95

 Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala
 100 105 110

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val
 115 120 125
 Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe
 130 135 140
 Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn
 145 150 155 160
 Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu
 165 170 175
 Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser
 180 185 190
 Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr
 195 200 205
 Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala
 210 215 220
 Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg
 225 230 235 240
 Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg
 245 250 255
 Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala
 260 265 270
 Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr
 275 280 285
 Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu
 290 295 300
 Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu
 305 310 315 320
 Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys
 325 330 335
 Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu
 340 345 350
 Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg
 355 360 365
 Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro
 370 375 380
 Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr
 385 390 395 400
 Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu
 405 410 415
 Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn
 420 425 430
 Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

435	440	445
Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr		
450	455	460
Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys		
465	470	475
Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys		
	485	490
Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn		
	500	505
Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn		
	515	520
		525

<210> 125

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA02432

<400> 125

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gtgcacataa caactgcagc tagttgatac gctagagcgc atg tcg aag cag cac 115
                                   Met Ser Lys Gln His
                                   1           5

tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163
Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys
               10               15               20

gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211
Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala
               25               30               35

aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259
Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro
               40               45               50

atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307
Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu
               55               60               65

atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355
Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser
               70               75               80               85

atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403
Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly
               90               95               100

gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451
Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

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105										110					115					
gta	gac	acc	ttc	ctt	gat	gat	ccc	cgc	cca	gtc	att	ttc	acc	ggc	gcc	499				
Val	Asp	Thr	Phe	Leu	Asp	Asp	Pro	Arg	Pro	Val	Ile	Phe	Thr	Gly	Ala					
		120						125					130							
caa	aaa	ccc	ttc	gat	cat	ccc	gaa	gcc	gac	ggc	cca	aac	aac	ctt	ttc	547				
Gln	Lys	Pro	Phe	Asp	His	Pro	Glu	Ala	Asp	Gly	Pro	Asn	Asn	Leu	Phe					
	135						140					145								
gaa	gcc	tgc	ctc	atc	gca	tcc	gac	ccc	tcc	gct	cgc	gga	att	ggt	gca	595				
Glu	Ala	Cys	Leu	Ile	Ala	Ser	Asp	Pro	Ser	Ala	Arg	Gly	Ile	Gly	Ala					
150					155					160					165					
ctc	att	gtc	ttc	ggc	cac	gcc	gtc	atc	cct	gct	cgc	ggc	tgc	gtt	aaa	643				
Leu	Ile	Val	Phe	Gly	His	Ala	Val	Ile	Pro	Ala	Arg	Gly	Cys	Val	Lys					
				170					175					180						
tgg	cac	acc	tct	gat	gag	ctg	gcg	ttt	gca	acc	aac	ggc	cct	gaa	gaa	691				
Trp	His	Thr	Ser	Asp	Glu	Leu	Ala	Phe	Ala	Thr	Asn	Gly	Pro	Glu	Glu					
			185					190					195							
cca	gag	cgc	ccc	gat	gcg	ctg	ccc	gta	gct	aaa	ttg	gcg	gat	gtc	tct	739				
Pro	Glu	Arg	Pro	Asp	Ala	Leu	Pro	Val	Ala	Lys	Leu	Ala	Asp	Val	Ser					
		200					205					210								
gtc	gaa	atc	atc	ccc	gca	tac	cct	ggc	gcc	acc	ggc	gca	atg	gtg	gaa	787				
Val	Glu	Ile	Ile	Pro	Ala	Tyr	Pro	Gly	Ala	Thr	Gly	Ala	Met	Val	Glu					
	215					220					225									
gct	gcc	atc	gct	gcc	ggc	gct	caa	gga	ctt	gta	gtg	gaa	gca	atg	gga	835				
Ala	Ala	Ile	Ala	Ala	Gly	Ala	Gln	Gly	Leu	Val	Val	Glu	Ala	Met	Gly					
230					235					240					245					
tca	ggc	aat	gtt	ggc	tcc	cgc	atg	ggc	gat	gcc	cta	ggc	aaa	gca	ctt	883				
Ser	Gly	Asn	Val	Gly	Ser	Arg	Met	Gly	Asp	Ala	Leu	Gly	Lys	Ala	Leu					
				250					255					260						
gac	gct	gga	att	ccc	gtg	gtg	atg	agc	act	agg	gtt	cct	cgt	ggc	gaa	931				
Asp	Ala	Gly	Ile	Pro	Val	Val	Met	Ser	Thr	Arg	Val	Pro	Arg	Gly	Glu					
			265					270					275							
gta	tcc	gga	gtg	tat	ggc	ggc	gca	ggc	gga	ggc	gcg	act	ttg	gct	gcg	979				
Val	Ser	Gly	Val	Tyr	Gly	Gly	Ala	Gly	Gly	Gly	Ala	Thr	Leu	Ala	Ala					
		280					285					290								
aag	ggc	gct	gtg	gga	tct	cgc	tac	ttc	aga	gct	ggc	cag	gca	cgt	att	1027				
Lys	Gly	Ala	Val	Gly	Ser	Arg	Tyr	Phe	Arg	Ala	Gly	Gln	Ala	Arg	Ile					
	295					300					305									
ttg	ctc	gcg	att	gcc	att	gcg	acg	ggc	gca	cat	ccg	gtg	acg	ctt	tac	1075				
Leu	Leu	Ala	Ile	Ala	Ile	Ala	Thr	Gly	Ala	His	Pro	Val	Thr	Leu	Tyr					
310					315					320					325					
taatttcgcc	cttggccttg	cat														1098				

<210> 126

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 126

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                20                      25                      30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
                35                      40                      45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
  50                      55                      60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
  65                      70                      75                      80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
                85                      90                      95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
                100                      105                      110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
  115                      120                      125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
  130                      135                      140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
  145                      150                      155                      160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
                165                      170                      175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
                180                      185                      190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
  195                      200                      205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
  210                      215                      220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
  225                      230                      235                      240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
                245                      250                      255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
                260                      265                      270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
                275                      280                      285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
  290                      295                      300

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Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His
 305 310 315 320

Pro Val Thr Leu Tyr
 325

<210> 127
 <211> 775
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXN03003

<400> 127
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 caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
 Met Thr Ser Arg Thr
 1 5
 ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20
 gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35
 gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50
 gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65
 gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145

atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165

 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180

 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195

 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
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 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
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<210> 128

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45

 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60

 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

 Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
 85 90 95

 Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
 100 105 110

 Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
 115 120 125

 Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
 130 135 140

 Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
 145 150 155 160

 Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
 165 170 175

 Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr

180	185	190
Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp		
195	200	205
Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser		
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Leu		
225		
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	Met Asn Leu Leu Thr	5
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acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163		
Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys		
10	15	20
caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211		
Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala		
25	30	35
tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259		
Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly		
40	45	50
gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307		
Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg		
55	60	65
gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355		
Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu		
70	75	80
cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403		
Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile		
90	95	100
tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451		
Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile		
105	110	115
cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499		
Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp		
120	125	130

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac	547
Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Ala Pro His	
135 140 145	
att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca	595
Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro	
150 155 160 165	
gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt	643
Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu	
170 175 180	
gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc	691
Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys	
185 190 195	
aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc	739
Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val	
200 205 210	
cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag	787
Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu	
215 220 225	
cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta	835
His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val	
230 235 240 245	
aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc	883
Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg	
250 255 260	
gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat	931
Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp	
265 270 275	
ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc	979
Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly	
280 285 290	
ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att	
1027	
Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile	
295 300 305	
tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg	
1075	
Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val	
310 315 320 325	
ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta	
1123	
Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu	
330 335 340	
gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc	
1171	
Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val	
345 350 355	

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 1206
 Arg Ala Tyr Val
 360

<210> 130
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 130

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			20					25					30		
Val	Lys	Ala	Asn	Ala	Tyr	Asn	His	Gly	Val	Glu	Lys	Val	Ala	Pro	Val
		35					40					45			
Ile	Ala	Ala	His	Gly	Ala	Asp	Ala	Phe	Gly	Val	Ala	Thr	Leu	Ala	Glu
		50				55					60				
Ala	Met	Gln	Leu	Arg	Asp	Ile	Gly	Ile	Ser	Gln	Glu	Val	Leu	Cys	Trp
65					70					75					80
Ile	Trp	Thr	Pro	Glu	Gln	Asp	Phe	Arg	Ala	Ala	Ile	Asp	Arg	Asn	Ile
				85					90					95	
Asp	Leu	Ala	Val	Ile	Ser	Pro	Ala	His	Ala	Lys	Ala	Leu	Ile	Glu	Thr
			100					105					110		
Asp	Ala	Glu	His	Ile	Arg	Val	Ser	Ile	Lys	Ile	Asp	Ser	Gly	Leu	His
		115					120					125			
Arg	Ser	Gly	Val	Asp	Glu	Gln	Glu	Trp	Glu	Gly	Val	Phe	Ser	Ala	Leu
	130					135					140				
Ala	Ala	Ala	Pro	His	Ile	Glu	Val	Thr	Gly	Met	Phe	Thr	His	Leu	Ala
145					150					155					160
Cys	Ala	Asp	Glu	Pro	Glu	Asn	Pro	Glu	Thr	Asp	Arg	Gln	Ile	Ile	Ala
				165				170					175		
Phe	Arg	Arg	Ala	Leu	Ala	Leu	Ala	Arg	Lys	His	Gly	Leu	Glu	Cys	Pro
			180					185					190		
Val	Asn	His	Val	Cys	Asn	Ser	Pro	Ala	Phe	Leu	Thr	Arg	Ser	Asp	Leu
		195					200					205			
His	Met	Glu	Met	Val	Arg	Pro	Gly	Leu	Ala	Phe	Tyr	Gly	Leu	Glu	Pro
	210					215					220				
Val	Ala	Gly	Leu	Glu	His	Gly	Leu	Lys	Pro	Ala	Met	Thr	Trp	Glu	Ala
225					230					235					240
Lys	Val	Ser	Val	Val	Lys	Gln	Ile	Glu	Ala	Gly	Gln	Gly	Thr	Ser	Tyr
			245						250					255	
Gly	Leu	Thr	Trp	Arg	Ala	Glu	Asp	Arg	Gly	Phe	Val	Ala	Val	Val	Pro

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<211> 1152
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101) .. (1129)
<223> RXN00636
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 105 110 115

gat atc aag gct ctg att gaa gtg gat tcg gga cat cgt aga agt gga 499
 Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly
 120 125 130

gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc 547
 Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly
 135 140 145

agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg 595
 Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro
 150 155 160 165

gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac 643
 Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn
 170 175 180

agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg 691
 Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro
 185 190 195

tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat 739
 Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr
 200 205 210

gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag 787
 Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys
 215 220 225

cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca 835
 Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser
 230 235 240 245

gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat 883
 Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp
 250 255 260

aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa 931
 Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu
 265 270 275

gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca 979
 Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro
 280 285 290

gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc
 1027
 Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro
 295 300 305

aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg
 1075
 Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg
 310 315 320 325

gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga
 1123



Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg
330 335 340

aac aat tagggaaacc tcttgacctt cac
1152
Asn Asn

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<210> 132
<211> 343
<212> PRT
<213> Corynebacterium glutamicum
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  1                               5           10           15
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Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala
20 25 30

Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met
35 40 45

Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu
50 55 60

Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr
65 70 75 80

Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro
85 90 95

Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr
100 105 110

Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly
115 120 125

His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile
130 135 140

Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly
145 150 155 160

His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu
165 170 175

Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser
180 185 190

Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met
195 200 205

Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly
210 215 220

Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val
225 230 235 240

Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys

245	250	255
Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val 260	265	270
Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala 275	280	285
Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln 290	295	300
Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp 305	310	315
Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val 325	330	335
Val Ala Arg Gly Arg Asn Asn 340		

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(856)
 <223> RXA02536

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 Met Asp Asn Phe Ala
 1 5
 ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
 10 15 20
 ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
 25 30 35
 gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
 40 45 50
 aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
 55 60 65
 cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
 70 75 80 85
 aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
 90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115
 ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130
 gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145
 gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165
 ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala
 170 175 180
 ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
 185 190 195
 gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
 200 205 210
 atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
 215 220 225
 cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
 230 235 240 245
 cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879
 Arg Glu Ala Leu Pro Val Leu
 250

<210> 134

<211> 252

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 134

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Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe
 20 25 30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
 35 40 45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
 50 55 60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr

65						70						75					80
Ile	Ser	Arg	Val	Asn	Asn	Thr	Val	Leu	Ile	Ser	Gly	Ala	Gly	Leu	His		
				85					90					95			
Gln	Gly	Tyr	Asn	Lys	Ile	His	Thr	Tyr	Asp	Ala	Phe	Gly	Tyr	Arg	Glu		
			100					105					110				
Ser	Asp	Thr	Val	Lys	Pro	Gly	Asp	Glu	Leu	Val	Val	Phe	Glu	Val	Asp		
		115					120					125					
Asp	Ile	Lys	Phe	Gly	Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu		
	130					135					140						
Gln	Phe	Lys	Asp	Leu	Ala	Arg	Asn	Gly	Ala	Gln	Ile	Ile	Val	Val	Pro		
145					150					155					160		
Thr	Ser	Trp	Gln	Asp	Gly	Pro	Gly	Lys	Leu	Glu	Gln	Trp	Glu	Val	Leu		
			165						170					175			
Pro	Arg	Ala	Arg	Ala	Leu	Asp	Ser	Thr	Cys	Trp	Ile	Val	Ala	Cys	Gly		
			180					185					190				
Gln	Ala	Arg	Leu	Pro	Glu	Glu	Leu	Arg	Asp	Glu	Arg	Lys	Gly	Pro	Thr		
		195					200					205					
Gly	Ile	Gly	His	Ser	Met	Val	Thr	Asn	Pro	His	Gly	Glu	Val	Ile	Ala		
	210					215					220						
Ser	Ala	Gly	Tyr	Glu	Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser		
225					230					235					240		
Gly	Leu	Ala	Lys	Ile	Arg	Glu	Ala	Leu	Pro	Val	Leu						
			245						250								

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 <213> Corynebacterium glutamicum
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 <222> (101)..(1612)
 <223> RXS00870
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 caacaattca cttcgcagag catttaagga atttacacac atg tct gaa cca caa 115
 Met Ser Glu Pro Gln
 1 5
 acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163
 Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
 10 15 20
 aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211
 Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
 25 30 35

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc	259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala	
40 45 50	
acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa	307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln	
55 60 65	
gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag	355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu	
70 75 80 85	
ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggg ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile
 280 285 290
 gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac
 1027
 Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp
 295 300 305
 acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac
 1075
 Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His
 310 315 320 325
 ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat
 1123
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
 330 335 340
 gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt
 1171
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
 345 350 355
 aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg
 1219
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
 360 365 370
 ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc
 1267
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
 375 380 385
 ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca
 1315
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
 390 395 400 405
 att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc
 1363
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe
 410 415 420
 acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg
 1411
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val
 425 430 435
 ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac
 1459
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
 440 445 450
 tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat
 1507
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
 455 460 465
 ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc
 1555
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser



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<210> 136
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
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Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
  20          25          30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
  35          40          45

Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
  50          55          60

Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
  65          70          75          80

Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
  85          90          95

Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
  100          105          110

Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
  115          120          125

Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
  130          135          140

Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met
  145          150          155          160

Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
  165          170          175

Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
  180          185          190

Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
  195          200          205

Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
  210          215          220

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Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
 225 230 235 240
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
 245 250 255
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
 260 265 270
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
 275 280 285
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
 290 295 300
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
 305 310 315 320
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
 325 330 335
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
 340 345 350
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe
 355 360 365
 Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala
 370 375 380
 Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala
 385 390 395 400
 Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn
 405 410 415
 Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln
 420 425 430
 His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val
 435 440 445
 Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly
 450 455 460
 Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu
 465 470 475 480
 Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile
 485 490 495
 Asn Leu Gly Phe Pro Gln Asn Asp
 500

<210> 137

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXS02299

<400> 137

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taaaacttgc aggacaaccc ccataaggac accacaggac atg ctg cgc acc atc 115
                                         Met Leu Arg Thr Ile
                                         1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
                        10 15 20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
                        25 30 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
                        40 45 50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile
                        55 60 65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
                        70 75 80 85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
                        90 95 100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
                        105 110 115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
                        120 125 130

aga agc att tagcgtttta gctcgccaat att 531
Arg Ser Ile
135

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<210> 138

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
1 5 10 15

Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
20 25 30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp

```

35	40	45	
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val	Ile Val Gly Asp Ala		
50	55	60	
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala His Leu Ile Asn			
65	70	75	80
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala			
	85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn			
	100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser			
	115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile			
130	135		
<210> 139			
<211> 1053			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1030)			
<223> RXA01561			
<400> 139			
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taataatggt cattttcatc gagttctaga aaacacaggc atg ctc acc ctc aac 115			
Met Leu Thr Leu Asn 5			
gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163			
Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr 20			
cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211			
Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys 35			
gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259			
Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe 50			
aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt 307			
Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val 65			
ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355			
Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe 85			
gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403			
Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr 100			

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gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg 451
Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val
105 110 115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc 499
Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr
120 125 130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547
Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro
135 140 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595
Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp
150 155 160 165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643
Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu
170 175 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691
Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val
185 190 195

gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739
Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
200 205 210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
215 220 225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
230 235 240 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
250 255 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
265 270 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
280 285 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca
1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
295 300 305

ctg tgatgtgatt tcaaacgata aca
1053
Leu
310

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<210> 140

<211> 310
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 140

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Met Leu Thr Leu Asn Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro
 1           5           10           15

His Val Arg Arg Thr Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr
          20           25           30

Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
          35           40           45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
 50           55           60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
 65           70           75           80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
          85           90           95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
          100          105          110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe
          115          120          125

Glu Ala Ala Gln Thr Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His
          130          135          140

Ala Tyr Asp Gln Pro Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu
          145          150          155          160

Glu Ile Val Glu Asp Leu Pro Asp Val Asp Thr Ile Val Val Ala Val
          165          170          175

Gly Gly Gly Gly Leu Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His
          180          185          190

Asp Ile Lys Val Val Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His
          195          200          205

Asn Ser Leu Ile Ala Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile
          210          215          220

Ala Ala Asp Ser Leu Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp
          225          230          235          240

Ile Ala Thr Ala His Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala
          245          250          255

Ile Ile Ala Ala Arg Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala
          260          265          270

Glu His Gly Ala Ala Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr
          275          280          285

Lys Pro Ala Ala Asp Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn
          290          295          300

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Thr Asp Leu Thr Thr Leu
305 310

<210> 141
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXA01850

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tcaccttgta caccaccaga gaaaaggccc accctcagcc atg gct atc agt gtt 115
Met Ala Ile Ser Val
1 5
gtt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc 163
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val
10 15 20
ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg 211
Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser
25 30 35
cat gtc gat atc acg ttg cac gga tcc ctt gcc gcc acc ggt aaa ggc 259
His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly
40 45 50
cac tgc act gac cgg gcg gta tta ctg ggt ctg gtg gga tgg gaa cca 307
His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro
55 60 65
acg ata gtt ccc att gat gct gca ccc tca ccc gcc gcg ccg att cct 355
Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro Gly Ala Pro Ile Pro
70 75 80 85
gcg aaa ggt tct gtg aac ggg cca aag gga acg gtg tcg tat tcc ctg 403
Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr Val Ser Tyr Ser Leu
90 95 100
acg ttt gat cct cat cct ctt cca gaa cac ccc aat gcc gtt acc ttt 451
Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe
105 110 115
aaa gga tca acc aca agg act tat ttg tcg gtg ggt ggt ggg ttc att 499
Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val Gly Gly Gly Phe Ile
120 125 130
atg acg ttg gag gat ttc cgg aag ctg gac gat atc gga tca ggt gtg 547
Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val
135 140 145
tca acc att cat cca gag gca gag gtg cct tgt cct ttt cag aag agt 595
Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys Pro Phe Gln Lys Ser
150 155 160 165

tcc caa tta ctc gca tat ggt cgc gat ttt gcg gag gtc atg aag gat	643
Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp	
170 175 180	
aat gag cgc tta atc cac ggg gat ctt ggc aca gtg gat gcc cat ttg	691
Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu	
185 190 195	
gat cga gtg tgg cag att atg cag gag tgc gtg gca caa ggc atc gca	739
Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val Ala Gln Gly Ile Ala	
200 205 210	
acg ccg ggg att tta ccg ggt ggg ttg aat gtg caa cgt cgg gcg ccg	787
Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro	
215 220 225	
cag gta cac gcg ctg att agc aac ggg gat acg tgt gag ctg ggt gct	835
Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala	
230 235 240 245	
gat ctt gat gct gtg gag tgg gtg aat ctg tac gcc ttg gcg gtg aat	883
Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn	
250 255 260	
gaa gaa aac gcc gct ggt ggt cgt gtg gtt act gct ccg act aat ggt	931
Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly	
265 270 275	
gct gcg ggg att att ccg gcg gtg atg cac tat gcg ccg gat ttt ttg	979
Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu	
280 285 290	
aca ggt ttt ggg gcg gag cag gcg cgg acg ttt ttg tat acc gcg ggt	
1027	
Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe Leu Tyr Thr Ala Gly	
295 300 305	
gcg gtg ggc atc atc att aag gaa aat gcc tcg atc tct ggc gcg gag	
1075	
Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu	
310 315 320 325	
gtg ggg tgt cag ggt gag gtt ggt tca gcg tcc gcg atg gcg gct gcc	
1123	
Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser Ala Met Ala Ala Ala	
330 335 340	
ggg ttg tgt gca gtc tta ggt ggt tct ccg caa cag gtg gaa aac gcc	
1171	
Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln Gln Val Glu Asn Ala	
345 350 355	
gcg gag att gcg ttg gag cac aat ttg gga ttg acg tgc gat ccg gtg	
1219	
Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val	
360 365 370	
ggc ggg tta gtg cag att ccg tgt att gaa cgc aac gct att gct gcc	
1267	
Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala Ile Ala Ala	

375 380 385
 atg aag tcc atc aat gcg gca agg ctt gcc cgg att ggt gat ggc aac
 1315
 Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn
 390 395 400 405

 aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc
 1363
 Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly
 410 415 420

 cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca
 1411
 Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala
 425 430 435

 acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcggtagc
 1457
 Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys
 440 445

 gctttaacac ggc
 1470

 <210> 142
 <211> 449
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 142
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 Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser
 20 25 30

 Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
 35 40 45

 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
 50 55 60

 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
 65 70 75 80

 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
 85 90 95

 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
 100 105 110

 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
 115 120 125

 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
 130 135 140

 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
 145 150 155 160

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
 165 170 175
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
 180 185 190
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
 195 200 205
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
 210 215 220
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
 225 230 235 240
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
 245 250 255
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
 260 265 270
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
 275 280 285
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
 290 295 300
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
 305 310 315 320
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
 325 330 335
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
 340 345 350
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu
 355 360 365
 Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg
 370 375 380
 Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg
 385 390 395 400
 Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr
 405 410 415
 Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser
 420 425 430
 Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu
 435 440 445

Cys

<210> 143
 <211> 1425



<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1402)  
<223> RXA00580
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				Met	Thr	Asp	Ala	His								5
				1												
caa	gcg	gac	gat	gtc	cgt	tac	cag	cca	ctg	aac	gag	ctt	gat	cct	gag	163
Gln	Ala	Asp	Asp	Val	Arg	Tyr	Gln	Pro	Leu	Asn	Glu	Leu	Asp	Pro	Glu	
				10					15					20		
gtg	gct	gct	gcc	atc	gct	ggg	gaa	ctt	gcc	cgt	caa	cgc	gat	aca	tta	211
Val	Ala	Ala	Ala	Ile	Ala	Gly	Glu	Leu	Ala	Arg	Gln	Arg	Asp	Thr	Leu	
				25				30					35			
gag	atg	atc	gcg	tct	gag	aac	ttc	gtt	ccc	cgt	tct	gtt	ttg	cag	gcg	259
Glu	Met	Ile	Ala	Ser	Glu	Asn	Phe	Val	Pro	Arg	Ser	Val	Leu	Gln	Ala	
				40			45						50			
cag	ggt	tct	gtt	ctt	acc	aat	aag	tat	gcc	gag	ggt	tac	cct	ggc	cgc	307
Gln	Gly	Ser	Val	Leu	Thr	Asn	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Gly	Arg	
							60					65				
cgt	tac	tac	ggt	ggt	tgc	gaa	caa	gtt	gac	atc	att	gag	gat	ctt	gca	355
Arg	Tyr	Tyr	Gly	Gly	Cys	Glu	Gln	Val	Asp	Ile	Ile	Glu	Asp	Leu	Ala	
					75					80					85	
cgt	gat	cgt	gcg	aag	gct	ctc	ttc	ggt	gca	gag	ttc	gcc	aat	gtt	cag	403
Arg	Asp	Arg	Ala	Lys	Ala	Leu	Phe	Gly	Ala	Glu	Phe	Ala	Asn	Val	Gln	
				90					95					100		
cct	cac	tct	ggc	gca	cag	gct	aat	gct	gct	gtg	ctg	atg	act	ttg	gct	451
Pro	His	Ser	Gly	Ala	Gln	Ala	Asn	Ala	Ala	Val	Leu	Met	Thr	Leu	Ala	
			105					110					115			
gag	cca	ggc	gac	aag	atc	atg	ggt	ctg	tct	ttg	gct	cat	ggt	ggt	cac	499
Glu	Pro	Gly	Asp	Lys	Ile	Met	Gly	Leu	Ser	Leu	Ala	His	Gly	Gly	His	
				120			125					130				
ttg	acc	cac	gga	atg	aag	ttg	aac	ttc	tcc	gga	aag	ctg	tac	gag	gtt	547
Leu	Thr	His	Gly	Met	Lys	Leu	Asn	Phe	Ser	Gly	Lys	Leu	Tyr	Glu	Val	
				135		140					145					
gtt	gcg	tac	ggt	gtt	gat	cct	gag	acc	atg	cgt	gtt	gat	atg	gat	cag	595
Val	Ala	Tyr	Gly	Val	Asp	Pro	Glu	Thr	Met	Arg	Val	Asp	Met	Asp	Gln	

185										190					195					
gct	gcg	gaa	gtt	ggc	gcg	aag	ctg	tgg	gtc	gat	atg	gct	cac	ttc	gct	739				
Ala	Ala	Glu	Val	Gly	Ala	Lys	Leu	Trp	Val	Asp	Met	Ala	His	Phe	Ala					
		200					205					210								
ggt	ctt	gtt	gct	gct	ggg	ttg	cac	cca	agc	cca	gtt	cct	tac	tct	gat	787				
Gly	Leu	Val	Ala	Ala	Gly	Leu	His	Pro	Ser	Pro	Val	Pro	Tyr	Ser	Asp					
	215					220					225									
ggt	gtt	tct	tcc	act	gtc	cac	aag	act	ttg	ggg	gga	cct	cgt	tcc	ggc	835				
Val	Val	Ser	Ser	Thr	Val	His	Lys	Thr	Leu	Gly	Gly	Pro	Arg	Ser	Gly					
230					235					240					245					
atc	att	ctg	gct	aag	cag	gag	tac	gcg	aag	aag	ctg	aac	tct	tcc	gta	883				
Ile	Ile	Leu	Ala	Lys	Gln	Glu	Tyr	Ala	Lys	Lys	Leu	Asn	Ser	Ser	Val					
				250					255					260						
ttc	cca	ggt	cag	cag	ggg	ggg	cct	ttg	atg	cac	gca	gtt	gct	gcg	aag	931				
Phe	Pro	Gly	Gln	Gln	Gly	Gly	Pro	Leu	Met	His	Ala	Val	Ala	Ala	Lys					
			265					270					275							
gct	act	tct	ttg	aag	att	gct	ggc	act	gag	cag	ttc	cgt	gac	cgt	cag	979				
Ala	Thr	Ser	Leu	Lys	Ile	Ala	Gly	Thr	Glu	Gln	Phe	Arg	Asp	Arg	Gln					
	280						285					290								
gct	cgc	acg	ttg	gag	ggg	gct	cgc	att	ctt	gct	gag	cgt	ctg	act	gct					
1027																				
Ala	Arg	Thr	Leu	Glu	Gly	Ala	Arg	Ile	Leu	Ala	Glu	Arg	Leu	Thr	Ala					
	295					300					305									
tct	gat	gcg	aag	gcc	gct	ggc	gtg	gat	gtc	ttg	acc	ggg	ggc	act	gat					
1075																				
Ser	Asp	Ala	Lys	Ala	Ala	Gly	Val	Asp	Val	Leu	Thr	Gly	Gly	Thr	Asp					
310				315						320				325						
gtg	cac	ttg	gtt	ttg	gct	gat	ctg	cgt	aac	tcc	cag	atg	gat	ggc	cag					
1123																				
Val	His	Leu	Val	Leu	Ala	Asp	Leu	Arg	Asn	Ser	Gln	Met	Asp	Gly	Gln					
				330					335					340						
cag	gcg	gaa	gat	ctg	ctg	cac	gag	gtt	ggg	atc	act	gtg	aac	cgt	aac					
1171																				
Gln	Ala	Glu	Asp	Leu	Leu	His	Glu	Val	Gly	Ile	Thr	Val	Asn	Arg	Asn					
			345					350					355							
gcg	gtt	cct	ttc	gat	cct	cgt	cca	cca	atg	gtt	act	tct	ggg	ctg	cgt					
1219																				
Ala	Val	Pro	Phe	Asp	Pro	Arg	Pro	Pro	Met	Val	Thr	Ser	Gly	Leu	Arg					
		360					365					370								
att	ggg	act	cct	gcg	ctg	gct	acc	cgt	ggg	ttc	gat	att	cct	gca	ttc					
1267																				
Ile	Gly	Thr	Pro	Ala	Leu	Ala	Thr	Arg	Gly	Phe	Asp	Ile	Pro	Ala	Phe					
	375					380					385									
act	gag	gtt	gca	gac	atc	att	ggg	act	gct	ttg	gct	aat	ggg	aag	tcc					
1315																				
Thr	Glu	Val	Ala	Asp	Ile	Ile	Gly	Thr	Ala	Leu	Ala	Asn	Gly	Lys	Ser					
390					395					400				405						

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat
1363

Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc
1412

Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val
425 430

tttgagtttt cat
1425

<210> 144

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn
1 5 10 15

Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg
20 25 30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys
165 170 175

Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp
195 200 205

Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro
210 215 220

Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly
 225 230 235 240
 Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys
 245 250 255
 Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His
 260 265 270
 Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln
 275 280 285
 Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala
 290 295 300
 Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu
 305 310 315 320
 Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser
 325 330 335
 Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile
 340 345 350
 Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val
 355 360 365
 Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe
 370 375 380
 Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu
 385 390 395 400
 Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala
 405 410 415
 Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr
 420 425 430
 Ile Val

<210> 145
 <211> 401
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1) .. (378)
 <223> RXA01821

<400> 145
 cga aac agc caa ggc aaa tgg tgc cca agt acg cga tca cca aaa aat 48
 Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
 1 5 10 15
 acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96
 Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

	20	25	30	
gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca				144
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr				
	35	40	45	
agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta				192
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu				
	50	55	60	
gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa				240
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu				
	65	70	75	80
aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga				288
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly				
	85	90	95	
gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag				336
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu				
	100	105	110	
tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg				378
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg				
	115	120	125	
tgatgtcctg atcccggttc cgg				401

<210> 146

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn				
1	5	10	15	
Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu				
20	25	30		
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr				
35	40	45		
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu				
50	55	60		
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu				
65	70	75	80	
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly				
85	90	95		
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu				
100	105	110		
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg				
115	120	125		

<210> 147



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<211> 488
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(478)
<223> RXN02263
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tgtgggaatc	acccgcactg	gcttgagaga	agaaacaaca	atg	aaa	att	gcg	gta							115		
				Met	Lys	Ile	Ala	Val									
									1						5		
atc	ggc	ctt	gga	tca	acc	ggc	tcc	atg	gca	ctg	tgg	cac	tta	agt	aac	163	
Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	Trp	His	Leu	Ser	Asn		
				10					15						20		
atc	cca	ggt	gta	gag	gcc	atc	ggc	ttt	gaa	caa	ttc	ggc	atc	tcc	cat	211	
Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	Phe	Gly	Ile	Ser	His		
			25					30						35			
ggc	tac	ggc	gca	ttc	aca	ggg	gag	tcc	cga	ctg	ttt	cgc	atg	gcc	tac	259	
Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	Phe	Arg	Met	Ala	Tyr		
		40					45						50				
cac	gaa	ggc	agc	acc	tac	gtt	ccg	ttg	ctc	aaa	cgc	gca	cga	gca	cta	307	
His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	Arg	Ala	Arg	Ala	Leu		
	55					60						65					
tgg	tca	tca	ctg	agc	gag	att	tcc	gga	cgc	gaa	ctc	ttc	cac	aac	ttc	355	
Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	Leu	Phe	His	Asn	Phe		
70					75						80					85	
ggt	gtc	tta	agc	acc	ggc	aag	gaa	gac	gaa	gca	ccc	ttc	caa	cgc	ctg	403	
Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Arg	Leu		
				90					95						100		
gtg	gaa	tca	gtg	gaa	cgt	tat	gag	ctg	cca	cat	gaa	cga	ctt	acc	gcc	451	
Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	Glu	Arg	Leu	Thr	Ala		
			105					110						115			
gcg	cag	atg	cgc	agc	gtt	acc	cag	gtc	tagacttccg							488	
Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val									
	120					125											

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<210> 148
<211> 126
<212> PRT
<213> Corynebacterium glutamicum
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<400> 148
Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
1 5 10 15
Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
20 25 30

Phe	Gly	Ile	Ser	His	Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu
		35					40					45			
Phe	Arg	Met	Ala	Tyr	His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys
	50					55					60				
Arg	Ala	Arg	Ala	Leu	Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu
65					70					75					80
Leu	Phe	His	Asn	Phe	Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala
				85					90					95	
Pro	Phe	Gln	Arg	Leu	Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His
			100					105					110		
Glu	Arg	Leu	Thr	Ala	Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val		
		115					120					125			

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<210> 149
<211> 460
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(460)  
<223> FRXA02263
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<400> 149																
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				Met	Lys	Ile	Ala	Val								
				1				5								
atc	ggc	ctt	gga	tca	acc	ggc	tcc	atg	gca	ctg	tgg	cac	tta	agt	aac	163
Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	Trp	His	Leu	Ser	Asn	
				10					15					20		
atc	cca	ggt	gta	gag	gcc	atc	ggc	ttt	gaa	caa	ttc	ggc	atc	tcc	cat	211
Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	Phe	Gly	Ile	Ser	His	
			25					30					35			
ggc	tac	ggc	gca	ttc	aca	ggg	gag	tcc	cga	ctg	ttt	cgc	atg	gcc	tac	259
Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	Phe	Arg	Met	Ala	Tyr	
		40					45					50				
cac	gaa	ggc	agc	acc	tac	gtt	ccg	ttg	ctc	aaa	cgc	gca	cga	gca	cta	307
His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	Arg	Ala	Arg	Ala	Leu	
	55					60					65					
tgg	tca	tca	ctg	agc	gag	att	tcc	gga	cgc	gaa	ctc	ttc	cac	aac	ttc	355
Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	Leu	Phe	His	Asn	Phe	
70					75					80					85	
ggt	gtc	tta	agc	acc	ggc	aag	gaa	gac	gaa	gca	ccc	ttc	caa	cgc	ctg	403
Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Arg	Leu	
				90					95					100		
gtg	gaa	tca	gtg	gaa	cgt	tat	gag	ctg	cca	cat	gaa	cga	ctt	acc	gcc	451



Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
 105 110 115

gcg cag atg
 Ala Gln Met
 120

460

<210> 150
 <211> 120
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 150
 Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
 1 5 10 15
 Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
 20 25 30
 Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
 35 40 45
 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
 50 55 60
 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
 65 70 75 80
 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
 85 90 95
 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
 100 105 110
 Glu Arg Leu Thr Ala Ala Gln Met
 115 120

<210> 151
 <211> 1251
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1228)
 <223> RXA02176

<400> 151
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 tggccctttt acttccaagc gcagaaagtt gcccgaaagac atg acc gac ttc ccc 115
 Met Thr Asp Phe Pro
 1 5
 acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163
 Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly
 10 15 20
 cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211

Pro	Ser	Lys	Val	Arg	Pro	Glu	Gln	Ile	Gln	Ala	Ile	Val	Asp	Gly	Ser		
			25					30					35				
gca	tcc	gtc	atc	ggg	acc	tca	cac	cgt	cag	ccg	gca	gta	aaa	aac	gtc	259	
Ala	Ser	Val	Ile	Gly	Thr	Ser	His	Arg	Gln	Pro	Ala	Val	Lys	Asn	Val		
		40					45					50					
gtg	ggg	tca	atc	cgc	gag	gga	ctc	tcc	gac	ctc	ttc	tcc	ctt	cca	gaa	307	
Val	Gly	Ser	Ile	Arg	Glu	Gly	Leu	Ser	Asp	Leu	Phe	Ser	Leu	Pro	Glu		
	55					60					65						
ggc	tac	gag	atc	atc	ctt	tcc	cta	ggg	ggg	gcg	acc	gca	ttc	tgg	gat	355	
Gly	Tyr	Glu	Ile	Ile	Leu	Ser	Leu	Gly	Gly	Ala	Thr	Ala	Phe	Trp	Asp		
70					75					80					85		
gca	gca	acc	ttc	gga	ctc	att	gaa	aag	aag	tcc	ggg	cac	ctt	tct	ttc	403	
Ala	Ala	Thr	Phe	Gly	Leu	Ile	Glu	Lys	Lys	Ser	Gly	His	Leu	Ser	Phe		
			90					95					100				
ggg	gag	ttc	tcc	tcc	aag	ttc	gca	aag	gct	tct	aag	ctt	gct	cct	tgg	451	
Gly	Glu	Phe	Ser	Ser	Lys	Phe	Ala	Lys	Ala	Ser	Lys	Leu	Ala	Pro	Trp		
		105						110				115					
ctc	gac	gag	cca	gag	atc	gtc	acc	gca	gaa	acc	ggg	gac	tct	ccg	gcc	499	
Leu	Asp	Glu	Pro	Glu	Ile	Val	Thr	Ala	Glu	Thr	Gly	Asp	Ser	Pro	Ala		
		120					125					130					
cca	cag	gca	ttc	gaa	ggc	gcc	gat	gtt	att	gca	tgg	gca	cac	aac	gaa	547	
Pro	Gln	Ala	Phe	Glu	Gly	Ala	Asp	Val	Ile	Ala	Trp	Ala	His	Asn	Glu		
		135				140					145						
acc	tcc	act	ggc	gcc	atg	gtt	cca	gtt	ctt	cgc	ccc	gaa	ggc	tct	gaa	595	
Thr	Ser	Thr	Gly	Ala	Met	Val	Pro	Val	Leu	Arg	Pro	Glu	Gly	Ser	Glu		
150					155					160					165		
ggc	tcc	ctg	gtt	gcc	att	gac	gca	acc	tcc	ggc	gct	ggg	gga	ctg	cca	643	
Gly	Ser	Leu	Val	Ala	Ile	Asp	Ala	Thr	Ser	Gly	Ala	Gly	Gly	Leu	Pro		
			170						175					180			
gta	gac	atc	aag	aac	tcc	gat	gtt	tac	tac	ttc	tcc	cca	cag	aag	tgc	691	
Val	Asp	Ile	Lys	Asn	Ser	Asp	Val	Tyr	Tyr	Phe	Ser	Pro	Gln	Lys	Cys		
			185					190					195				
ttc	gca	tcc	gac	ggg	ggc	ctg	tgg	ctt	gca	gcg	atg	agc	cca	gca	gct	739	
Phe	Ala	Ser	Asp	Gly	Gly	Leu	Trp	Leu	Ala	Ala	Met	Ser	Pro	Ala	Ala		
		200					205					210					
ctc	gag	cgc	atc	gag	aag	atc	aac	gct	tcc	gat	cgc	ttc	atc	cct	gag	787	
Leu	Glu	Arg	Ile	Glu	Lys	Ile	Asn	Ala	Ser	Asp	Arg	Phe	Ile	Pro	Glu		
		215				220					225						
ttc	ctc	aac	ctg	cag	acc	gca	gtg	gat	aac	tcc	ctg	aag	aac	cag	acc	835	
Phe	Leu	Asn	Leu	Gln	Thr	Ala	Val	Asp	Asn	Ser	Leu	Lys	Asn	Gln	Thr		
230					235					240				245			
tac	aac	acc	cca	gct	gtt	gct	acc	ttg	ctg	atg	ctg	gac	aac	cag	gtc	883	
Tyr	Asn	Thr	Pro	Ala	Val	Ala	Thr	Leu	Leu	Met	Leu	Asp	Asn	Gln	Val		
			250					255						260			
aag	tgg	atg	aac	tcc	aac	ggc	ggc	ctg	gat	gga	atg	gtt	gct	cgc	acc	931	
Lys	Trp	Met	Asn	Ser	Asn	Gly	Gly	Leu	Asp	Gly	Met	Val	Ala	Arg	Thr		



265 270 275
 aca gca agc tcc tcc gcc ctg tac aac tgg gct gag gct cgc gag gag 979
 Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala Glu Ala Arg Glu Glu
 280 285 290
 gca tcc cca tac gtg gca gat gca gct aag cgc tcc ctc gtt gtc ggc
 1027
 Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg Ser Leu Val Val Gly
 295 300 305
 acc atc gac ttc gat gac tcc atc gac gca gca gtg atc gct aag ata
 1075
 Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala Val Ile Ala Lys Ile
 310 315 320 325
 ctg cgc gca aac ggc atc ctg gac acc gag cct tac cgc aag ctg gga
 1123
 Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro Tyr Arg Lys Leu Gly
 330 335 340
 cgc aac cag ctg cgc atc ggt atg ttc cca gcg atc gat tcc acc gat
 1171
 Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala Ile Asp Ser Thr Asp
 345 350 355
 gtg gaa aag ctc acc gga gca atc gac ttc atc ctc gat ggc ggt ttt
 1219
 Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile Leu Asp Gly Gly Phe
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 1251
 Ala Arg Lys
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 <213> Corynebacterium glutamicum
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 Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
 20 25 30
 Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
 35 40 45
 Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
 50 55 60
 Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
 65 70 75 80
 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
 85 90 95

Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
 100 105 110
 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr
 115 120 125
 Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala
 130 135 140
 Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg
 145 150 155 160
 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly
 165 170 175
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe
 180 185 190
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
 195 200 205
 Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp
 210 215 220
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser
 225 230 235 240
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met
 245 250 255
 Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly
 260 265 270
 Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala
 275 280 285
 Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg
 290 295 300
 Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala
 305 310 315 320
 Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro
 325 330 335
 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
 340 345 350
 Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile
 355 360 365
 Leu Asp Gly Gly Phe Ala Arg Lys
 370 375

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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 <222> (101) .. (1399)
 <223> RXN02758

<400> 153

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                                   Val Thr Glu Leu Ile
                                   1                               5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
                                   10                               15                               20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
                                   25                               30                               35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
                                   40                               45                               50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
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aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
                                   70                               75                               80                               85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                                   90                               95                               100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
                                   105                               110                               115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
                                   120                               125                               130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
                                   135                               140                               145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
                                   150                               155                               160                               165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
                                   170                               175                               180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt 691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly
                                   185                               190                               195

ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg 739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr

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200	205	210	
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gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu 230 235 240 245			835
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu 250 255 260			883
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro 265 270 275			931
ggg gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr 280 285 290			979
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 1027 Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu 295 300 305			
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 1075 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp 310 315 320 325			
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 1123 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala 330 335 340			
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 1171 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met 345 350 355			
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 1219 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu 360 365 370			
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 1267 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys 375 380 385			
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 1315 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu 390 395 400 405			
cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 1363 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu 410 415 420			

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg

1409

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425

430

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1422

<210> 154

<211> 433

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 154

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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
225 230 235 240

Ala

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<220>  
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<223> FRXA02479
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Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
10 15 20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
 25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
 40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
 55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
 70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
 Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
 90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
 Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
 105 110 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat 490
 Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
 120 125 130

<210> 156

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 156

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp
 130



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<210> 157
<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA02758
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Met Gly Tyr Gln Thr																5
1																
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag																163
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu																20
10 15																
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat																211
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp																35
25 30																
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg																259
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala																50
40 45																
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg																307
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met																65
55 60																
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc																355
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu																85
70 75 80																
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag																403
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys																100
90 95																
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg																451
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu																115
105 110																
cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa																499
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu																130
120 125																
gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcgc																545
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala																145
135 140 145																
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<210> 158
<211> 145
<212> PRT
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<213> Corynebacterium glutamicum

<400> 158

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
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Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
20 25 30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
35 40 45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
50 55 60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
65 70 75 80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
85 90 95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
100 105 110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
115 120 125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
130 135 140

Ala
145

<210> 159

<211> 205

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (72)..(182)

<223> FRXA02759

<400> 159

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aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
1 5 10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
15 20 25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
Val Thr Glu Arg Ala Met Arg Gly
30 35

<210> 160



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<211> 37
<212> PRT
<213> Corynebacterium glutamicum
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<400> 160

Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met
1 5 10 15

Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu
20 25 30

Arg Ala Met Arg Gly
35

<210> 161

<211> 1188

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) . . (1165)

<223> RXA02501

<400> 161

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gtctgtgcgc tcatgaacca ggaaggtttt tgtttgtctc atg agc tct gaa gga 115
Met Ser Ser Glu Gly
1 5

aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163
Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe
10 15 20

ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211
Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu
25 30 35

gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259
Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly
40 45 50

gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307
Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu
55 60 65

aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355
Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser
70 75 80 85

gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403
Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp
90 95 100

gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451
Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly
105 110 115

tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499

Ser	Ser	Leu	Ile	Val	Phe	Ala	Gln	Gly	Leu	Phe	Arg	Lys	Lys	Phe	Phe		
		120					125					130					
acc	atc	aaa	gaa	atc	ctc	ccc	gtg	gtg	tgg	aaa	caa	gtg	aaa	ttc	aaa	547	
Thr	Ile	Lys	Glu	Ile	Leu	Pro	Val	Val	Trp	Lys	Gln	Val	Lys	Phe	Lys		
		135				140					145						
ctc	acc	ggc	tcc	gaa	aac	gcc	gac	gac	gtc	tcc	cgc	ggc	cgc	gaa	caa	595	
Leu	Thr	Gly	Ser	Glu	Asn	Ala	Asp	Asp	Val	Ser	Arg	Gly	Arg	Glu	Gln		
150					155					160					165		
gcc	ctc	gaa	ttc	atc	aaa	ggc	cgc	ccc	gtc	caa	gaa	cta	gtt	gac	ctc	643	
Ala	Leu	Glu	Phe	Ile	Lys	Gly	Arg	Pro	Val	Gln	Glu	Leu	Val	Asp	Leu		
				170					175					180			
tgc	gaa	gaa	atc	gtc	gac	caa	cgc	atg	gcc	gac	aaa	atg	tgg	ccc	ggc	691	
Cys	Glu	Glu	Ile	Val	Asp	Gln	Arg	Met	Ala	Asp	Lys	Met	Trp	Pro	Gly		
			185					190					195				
acc	aaa	caa	ctc	gcc	gac	atg	cac	atc	gcc	gcc	ggc	cac	caa	gtc	tgg	739	
Thr	Lys	Gln	Leu	Ala	Asp	Met	His	Ile	Ala	Ala	Gly	His	Gln	Val	Trp		
		200					205					210					
ctc	gtc	tcc	gca	acc	ccc	gtc	caa	ctc	gcc	caa	atc	ctg	gca	caa	cgc	787	
Leu	Val	Ser	Ala	Thr	Pro	Val	Gln	Leu	Ala	Gln	Ile	Leu	Ala	Gln	Arg		
	215					220					225						
ctc	ggc	ttc	acc	gga	gcg	atc	ggc	aca	gtc	gca	gaa	gca	aaa	gat	gga	835	
Leu	Gly	Phe	Thr	Gly	Ala	Ile	Gly	Thr	Val	Ala	Glu	Ala	Lys	Asp	Gly		
230					235				240					245			
gta	ttc	acc	ggc	cga	ctc	gtc	ggc	gac	atc	ctc	cac	gga	ccc	ggc	aaa	883	
Val	Phe	Thr	Gly	Arg	Leu	Val	Gly	Asp	Ile	Leu	His	Gly	Pro	Gly	Lys		
				250				255						260			
aga	cac	gca	gtc	gca	gca	ctc	gca	tcc	atc	gaa	caa	ctc	gac	ctc	acc	931	
Arg	His	Ala	Val	Ala	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Leu	Asp	Leu	Thr		
			265					270					275				
cga	tgc	acc	ggc	tac	tcc	gac	tcc	atc	aac	gac	ctc	ccc	atg	ctc	tcc	979	
Arg	Cys	Thr	Ala	Tyr	Ser	Asp	Ser	Ile	Asn	Asp	Leu	Pro	Met	Leu	Ser		
		280				285						290					
atg	gtc	ggc	acc	gcc	gtc	gca	gta	aac	ccc	gac	tcc	aaa	ctc	cgc	aaa		
1027																	
Met	Val	Gly	Thr	Ala	Val	Ala	Val	Asn	Pro	Asp	Ser	Lys	Leu	Arg	Lys		
	295					300					305						
gaa	gcc	gaa	acc	cga	ggc	tgg	gac	gtc	cgc	gat	ttc	cga	agc	atc	cgc		
1075																	
Glu	Ala	Glu	Thr	Arg	Gly	Trp	Asp	Val	Arg	Asp	Phe	Arg	Ser	Ile	Arg		
310					315				320					325			
aaa	gcc	acc	cgc	gaa	tac	gga	atc	ccc	gcc	ctg	gtc	acc	gcc	gca	ttc		
1123																	
Lys	Ala	Thr	Arg	Glu	Tyr	Gly	Ile	Pro	Ala	Leu	Val	Thr	Ala	Ala	Phe		
				330				335					340				
agt	gtc	gcc	ggc	tgg	agt	cta	cgc	cgc	cga	tgg	aga	aaa	caa				
1165																	
Ser	Val	Ala	Gly	Trp	Ser	Leu	Arg	Arg	Arg	Trp	Arg	Lys	Gln				



345

350

355

taacgcacag gagccgtttt aag
1188

<210> 162

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly
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Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu
20 25 30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala
35 40 45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile
50 55 60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala
65 70 75 80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro
85 90 95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn
100 105 110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe
115 120 125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys
130 135 140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser
145 150 155 160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln
165 170 175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp
180 185 190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala
195 200 205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln
210 215 220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala
225 230 235 240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu
245 250 255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu



260	265	270
Gln Leu Asp Leu Thr Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp 275 280 285		
Leu Pro Met Leu Ser Met Val Gly Thr Ala Val Ala Val Asn Pro Asp 290 295 300		
Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp 305 310 315 320		
Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu 325 330 335		
Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp 340 345 350		
Arg Lys Gln 355		
<210> 163		
<211> 558		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(535)		
<223> RXN03105		
<400> 163		
gggtggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60		
aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115		
		Leu Ile Leu Pro Val 5
		1
cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163		
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile		10 15 20
ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211		
Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu		25 30 35
gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259		
Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe		40 45 50
ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307		
Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr		55 60 65
tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355		
Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile		70 75 80 85
gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403		
Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr		90 95 100

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr
 105 110 115

 agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys
 120 125 130

 acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe
 135 140 145

 atctaacgct gag 558

<210> 164
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 164
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
 1 5 10 15

 His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp
 20 25 30

 Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys
 35 40 45

 Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser
 50 55 60

 Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala
 65 70 75 80

 Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys
 85 90 95

 Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn
 100 105 110

 Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro
 115 120 125

 Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg
 130 135 140

 Phe
 145

<210> 165
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (62)..(664)

<223> RXS01130

<400> 165

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agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1             5             10             15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
             20             25             30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
             35             40             45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
             50             55             60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
             65             70             75             80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
             85             90             95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
             100             105             110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
             115             120             125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
             130             135             140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
             145             150             155             160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
             165             170             175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
             180             185             190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
             195             200

tga 687

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<210> 166

<211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 166

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1           5           10           15
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20           25           30
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35           40           45
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50           55           60
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65           70           75           80
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85           90           95
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100          105          110
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115          120          125
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130          135          140
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
          145          150          155          160
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165          170          175
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180          185          190
Ala Thr Ser Phe Gln Val Asp Leu Asp
          195          200

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<210> 167
 <211> 604
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS03112

<400> 167

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gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgacgac 60
gctgcgtgag ggcgagtgga agcggctcttc tttcaacggg gtg gaa att ttc gga 115
                               Val Glu Ile Phe Gly
                               1           5

```



```

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
          10                      15                      20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
          25                      30                      35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
          40                      45                      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
          55                      60                      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
          70                      75                      80                      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
          90                      95                      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
          105                      110                      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
          120                      125                      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
          135                      140                      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
          150                      155                      160                      165

gcg ctg gct
Ala Leu Ala
904

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<210> 168
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

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<400> 168
Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1              5              10              15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
          20              25              30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
          35              40              45

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Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
 50 55 60
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
 65 70 75 80
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
 85 90 95
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160
 Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 169
 <211> 1458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1435)
 <223> RXN00969

<400> 169
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 taggacaaca acgctcgacc gcgattatatt ttggagaatc atg acc tca gca tct 115
 Met Thr Ser Ala Ser
 1 5
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
 10 15 20
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
 25 30 35
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
 40 45 50
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
 55 60 65
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
 70 75 80 85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt	403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg	
90 95 100	
gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc	451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala	
105 110 115	
aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg	499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala	
120 125 130	
gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca	547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala	
135 140 145	
att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc	595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile	
150 155 160 165	
cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac	643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp	
170 175 180	
gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca	691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala	
185 190 195	
act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc	739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly	
200 205 210	
cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac	787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His	
215 220 225	
acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc	835
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile	
230 235 240 245	
aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag	883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys	
250 255 260	
ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct	931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala	
265 270 275	
att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg	979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu	
280 285 290	
gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca	
1027	
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala	
295 300 305	
gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc	
1075	
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr	

310 315 320 325
 gcg tct gct gtg ctt ggc gac gtc gtt ggt gcc gca cga aac aag gtg
 1123
 Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala Ala Arg Asn Lys Val
 330 335 340
 cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc
 1171
 His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile
 345 350 355
 gct gat ttc ggt gag acc acc act cgt tac cac ctc gac atg gat gtg
 1219
 Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val
 360 365 370
 gaa gat cgc gtg ggg gtt ttg gct gaa ttg gct agc ctg ttc tct gag
 1267
 Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu
 375 380 385
 caa gga atc tcc ctg cgt aca atc cga cag gaa gag cgc gat gat gat
 1315
 Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp
 390 395 400 405
 gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc
 1363
 Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser
 410 415 420
 cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac
 1411
 Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn
 425 430 435
 agt gtg atc cgc ctc gaa agg gac taattttact gacatggcaa ttg
 1458
 Ser Val Ile Arg Leu Glu Arg Asp
 440 445

 <210> 170
 <211> 445
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 170
 Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly
 1 5 10 15
 Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu
 20 25 30
 Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
 35 40 45
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
 50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125
 Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
 130 135 140
 Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu
 145 150 155 160
 Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr
 165 170 175
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp
 180 185 190
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
 195 200 205
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
 210 215 220
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu
 225 230 235 240
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala
 245 250 255
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys
 260 265 270
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro
 275 280 285
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe
 290 295 300
 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
 305 310 315 320
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala
 325 330 335
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr
 340 345 350
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His
 355 360 365
 Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala
 370 375 380
 Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu



385					390					395					400
Glu	Arg	Asp	Asp	Asp	Ala	Arg	Leu	Ile	Val	Val	Thr	His	Ser	Ala	Leu
				405					410					415	
Glu	Ser	Asp	Leu	Ser	Arg	Thr	Val	Glu	Leu	Leu	Lys	Ala	Lys	Pro	Val
			420					425					430		
Val	Lys	Ala	Ile	Asn	Ser	Val	Ile	Arg	Leu	Glu	Arg	Asp			
		435					440					445			
 <210> 171															
<211> 493															
<212> DNA															
<213> Corynebacterium glutamicum															
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<221> CDS															
<222> (101)..(493)															
<223> FRXA00974															
 <400> 171															
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taggacaaca acgctcgacc gcgattatct ttggagaatc atg acc tca gca tct 115															
Met Thr Ser Ala Ser 5															
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163															
Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile 20															
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211															
Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met 35															
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259															
Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu 50															
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307															
Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val 65															
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355															
Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu 85															
 gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403															
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg 100															
 gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451															
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala 115															
 aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat 493															
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp 130															



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<210> 172
<211> 131
<212> PRT
<213> Corynebacterium glutamicum
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<400> 172
Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly
  1          5          10          15

Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu
      20          25          30

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
      35          40          45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
  50          55          60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
  65          70          75          80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
      85          90          95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
      100          105          110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
      115          120          125

Leu Ala Asp
    130

```

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<210> 173
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1027)
<223> RXA00970
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<400> 173
gaatctgac tttccgcac cgttgaactg ctgaaggcta agcctgttgt taaggcaatc 60

aacagtgtga tccgcctcga aagggactaa ttttactgac atg gca att gaa ctg 115
                                         Met Ala Ile Glu Leu
                                         1                               5

aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163
Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn
                        10                               15                               20

ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211
Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp
                        25                               30                               35

act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259

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Thr	Val	Glu	Val	Glu	Ile	Ile	Pro	Ser	Gly	Leu	Glu	Val	Glu	Val	Phe	
		40					45					50				
ggc	gaa	ggc	caa	ggc	gaa	gtc	cct	ctt	gat	ggc	tcc	cac	ctg	gtg	gtt	307
Gly	Glu	Gly	Gln	Gly	Glu	Val	Pro	Leu	Asp	Gly	Ser	His	Leu	Val	Val	
	55					60					65					
aaa	gct	att	cgt	gct	ggc	ctg	aag	gca	gct	gac	gct	gaa	gtt	cct	gga	355
Lys	Ala	Ile	Arg	Ala	Gly	Leu	Lys	Ala	Ala	Asp	Ala	Glu	Val	Pro	Gly	
	70				75					80					85	
ttg	cga	gtg	gtg	tgc	cac	aac	aac	att	ccg	cag	tct	cgt	ggc	ctt	ggc	403
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Ser	Ser	Ala	Ala	Ala	Ala	Val	Ala	Gly	Val	Ala	Ala	Ala	Asn	Gly	Leu	
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Ala	Asp	Phe	Pro	Leu	Thr	Gln	Glu	Gln	Ile	Val	Gln	Leu	Ser	Ser	Ala	
		120					125					130				
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Phe	Glu	Gly	His	Pro	Asp	Asn	Ala	Ala	Ala	Ser	Val	Leu	Gly	Gly	Ala	
	135					140					145					
gtg	gtg	tcg	tgg	aca	aat	ctg	tct	atc	gac	ggc	aag	agc	cag	cca	cag	595
Val	Val	Ser	Trp	Thr	Asn	Leu	Ser	Ile	Asp	Gly	Lys	Ser	Gln	Pro	Gln	
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Tyr	Ala	Ala	Val		Pro	Leu	Glu	Val	Gln	Asp	Asn	Ile	Arg	Ala	Thr	
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ctg	gtt	cct	aat	ttc	cac	gca	tcc	acc	gaa	gct	gtg	cgc	cga	gtc	ctt	691
Leu	Val	Pro	Asn	Phe	His	Ala	Ser	Thr	Glu	Ala	Val	Arg	Arg	Val	Leu	
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ccc	act	gaa	gtc	act	cac	atc	gat	gcg	cga	ttt	aac	gtg	tcc	cgc	gtt	739
Pro	Thr	Glu	Val	Thr	His	Ile	Asp	Ala	Arg	Phe	Asn	Val	Ser	Arg	Val	
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Ala	Val	Met	Ile	Val	Ala	Leu	Gln	Gln	Arg	Pro	Asp	Leu	Leu	Trp	Glu	
	215					220					225					
ggc	act	cgt	gac	cgt	ctg	cac	cag	cct	tat	cgt	gca	gaa	gtg	ttg	cct	835
Gly	Thr	Arg	Asp	Arg	Leu	His	Gln	Pro	Tyr	Arg	Ala	Glu	Val	Leu	Pro	
	230				235					240					245	
att	acc	tct	gag	tgg	gta	aac	cgc	ctg	cgc	aac	cgt	ggc	tac	gcg	gca	883
Ile	Thr	Ser	Glu	Trp	Val	Asn	Arg	Leu	Arg	Asn	Arg	Gly	Tyr	Ala	Ala	
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tac	ctt	tcc	ggc	gcc	ggc	cca	acc	gcc	atg	gtg	ctg	tcc	act	gag	cca	931
Tyr	Leu	Ser	Gly	Ala	Gly	Pro	Thr	Ala	Met	Val	Leu	Ser	Thr	Glu	Pro	
			265					270					275			
att	cca	gac	aag	gtt	ttg	gaa	gat	gct	cgt	gag	tct	ggc	att	aag	gtg	979
Ile	Pro	Asp	Lys	Val	Leu	Glu	Asp	Ala	Arg	Glu	Ser	Gly	Ile	Lys	Val	



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1027

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1050

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<212> PRT
<213> *Corynebacterium glutamicum*

<400> 174

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35 40 45

Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly
50 55 60

Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp
65 70 75 80

Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln
85 90 95

Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Val Ala Gly Val Ala
100 105 110

Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val
115 120 125

Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
130 135 140

Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly
145 150 155 160

Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn
165 170 175

Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala
180 185 190

Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe
195 200 205

Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro
210 215 220

Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg
225 230 235 240



Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn
 245 250 255

Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val
 260 265 270

Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu
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Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val
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Glu Val Asn Gln Pro
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 <223> RXA00330

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 Val Asp Tyr Ile Ser
 1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163
 Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu
 10 15 20

ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211
 Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro
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caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259
 Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn
 40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307
 Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp
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gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355
 Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr
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 Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu
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gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451
 Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe
 105 110 115

aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt	499
Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu	
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cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat	547
Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp	
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Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg	
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Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala	
170 175 180	
cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac	691
Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp	
185 190 195	
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Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp	
200 205 210	
gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac	787
Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn	
215 220 225	
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Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile	
230 235 240 245	
cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc	883
Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr	
250 255 260	
ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga	931
Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly	
265 270 275	
ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc	979
Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu	
280 285 290	
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1027	
Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val Arg Ser Ser Ala Asp	
295 300 305	
acc cac gag acc tcc tca cct tcg atg gat atc tcc cgc gcc tcc aac	
1075	
Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn	
310 315 320 325	
ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc	
1123	
Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val	
330 335 340	



aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct
1171

Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala
345 350 355

gat gac gcc aac ttt gag aag gct gca gca gaa tac ggt ttc gcc tcc
1219

Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser
360 365 370

gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat
1267

Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His
375 380 385

tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac
1315

Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His
390 395 400 405

gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta
1363

Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu
410 415 420

gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att
1411

Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile
425 430 435

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct
1459

Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala
440 445 450

cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag
1507

Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln
455 460 465

tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt
1553

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1566

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 35 40 45
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile
 50 55 60
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr
 65 70 75 80
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro
 85 90 95
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly
 100 105 110
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
 115 120 125
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly
 130 135 140
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
 145 150 155 160
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
 165 170 175
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe
 180 185 190
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
 195 200 205
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala
 210 215 220
 Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr
 225 230 235 240
 Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser
 245 250 255
 Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
 260 265 270
 Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
 275 280 285
 Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val
 290 295 300
 Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile
 305 310 315 320
 Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg
 325 330 335
 Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly
 340 345 350
 Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu



355					360					365					
Tyr	Gly	Phe	Ala	Ser	Gly	Arg	Ser	Thr	His	Ala	Asp	Arg	Val	Ala	Thr
	370					375					380				
Ile	Ala	Asp	Val	His	Ser	Arg	Leu	Asp	Val	Leu	Ile	Asp	Pro	His	Thr
385					390					395					400
Ala	Asp	Gly	Val	His	Val	Ala	Arg	Gln	Trp	Arg	Asp	Glu	Val	Asn	Thr
				405					410					415	
Pro	Ile	Ile	Val	Leu	Glu	Thr	Ala	Leu	Pro	Val	Lys	Phe	Ala	Asp	Thr
			420					425					430		
Ile	Val	Glu	Ala	Ile	Gly	Glu	Ala	Pro	Gln	Thr	Pro	Glu	Arg	Phe	Ala
		435					440					445			
Ala	Ile	Met	Asp	Ala	Pro	Phe	Lys	Val	Ser	Asp	Leu	Pro	Asn	Asp	Thr
	450					455					460				
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				Met	Pro	Thr	Leu	Ala								
				1				5								
cct	tca	ggt	caa	ctt	gaa	atc	caa	gcg	atc	ggt	gat	gtc	tcc	acc	gaa	163
Pro	Ser	Gly	Gln	Leu	Glu	Ile	Gln	Ala	Ile	Gly	Asp	Val	Ser	Thr	Glu	
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gcc	gga	gca	atc	att	aca	aac	gct	gaa	atc	gcc	tat	cac	cgc	tgg	ggt	211
Ala	Gly	Ala	Ile	Ile	Thr	Asn	Ala	Glu	Ile	Ala	Tyr	His	Arg	Trp	Gly	
			25					30					35			
gaa	tac	cgc	gta	gat	aaa	gaa	gga	cgc	agc	aat	gtc	ggt	ctc	atc	gaa	259
Glu	Tyr	Arg	Val	Asp	Lys	Glu	Gly	Arg	Ser	Asn	Val	Val	Leu	Ile	Glu	
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cac	gcc	ctc	act	gga	gat	tcc	aac	gca	gcc	gat	tgg	tgg	gct	gac	ttg	307
His	Ala	Leu	Thr	Gly	Asp	Ser	Asn	Ala	Ala	Asp	Trp	Trp	Ala	Asp	Leu	
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ctc	qgt	ccc	ggc	aaa	gcc	atc	aac	act	gat	att	tac	tgc	gtg	atc	tgt	355

Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys	
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acc	aac	gtc	atc	ggg	ggg	tgc	aac	ggg	tcc	acc	gga	cct	ggc	tcc	atg	403
Thr	Asn	Val	Ile	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Gly	Ser	Met	
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cat	cca	gat	gga	aat	ttc	tgg	ggg	aat	cgc	ttc	ccc	gcc	acg	tcc	att	451
His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe	Pro	Ala	Thr	Ser	Ile	
			105					110					115			
cgt	gat	cag	gta	aac	gcc	gaa	aaa	caa	ttc	ctc	gac	gca	ctc	ggc	atc	499
Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu	Asp	Ala	Leu	Gly	Ile	
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Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met	Gly	Gly	Ala	Arg	Thr	
		135				140						145				
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Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val	
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Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln	Ile	Gly	Ile	Gln	Ser	
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			185					190					195			
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Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Arg	
		200					205					210				
cgc	atc	gcc	cac	ctc	acc	tac	cgt	ggc	gaa	cta	gaa	atc	gac	gaa	cgc	787
Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu	Glu	Ile	Asp	Glu	Arg	
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Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro	Leu	Gly	Pro	Tyr	Arg	
230					235					240					245	
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Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr	Leu	Asp	Tyr	Gln	Ala	
			250						255					260		
gac	aag	cta	gta	cag	cgt	ttc	gac	gcc	ggc	tcc	tac	gtc	ttg	ctc	acc	931
Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser	Tyr	Val	Leu	Leu	Thr	
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gac	gcc	ctc	aac	cgc	cac	gac	att	ggg	cgc	gac	cgc	gga	ggc	ctc	aac	979
Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp	Arg	Gly	Gly	Leu	Asn	
		280					285					290				
aag	gca	ctc	gaa	tcc	atc	aaa	gtt	cca	gtc	ctt	gtc	gca	ggc	gta	gat	
1027																
Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu	Val	Ala	Gly	Val	Asp	
	295					300						305				

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1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
310 315 320 325

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1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
345 350 355

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1219
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
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35 40 45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140
Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160



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Trp	His	Glu 195	Gly	Asn	Tyr	Tyr	Glu 200	Ser	Gly	Cys	Asn	Pro 205	Ala	Thr	Gly
Leu	Gly 210	Ala	Ala	Arg	Arg	Ile 215	Ala	His	Leu	Thr	Tyr 220	Arg	Gly	Glu	Leu
Glu 225	Ile	Asp	Glu	Arg	Phe 230	Gly	Thr	Lys	Ala	Gln 235	Lys	Asn	Glu	Asn	Pro 240
Leu	Gly	Pro	Tyr	Arg 245	Lys	Pro	Asp	Gln 250	Arg	Phe	Ala	Val	Glu	Ser 255	Tyr
Leu	Asp	Tyr	Gln 260	Ala	Asp	Lys	Leu	Val 265	Gln	Arg	Phe	Asp	Ala 270	Gly	Ser
Tyr	Val 275	Leu	Leu	Thr	Asp	Ala	Leu 280	Asn	Arg	His	Asp	Ile 285	Gly	Arg	Asp
Arg	Gly 290	Gly	Leu	Asn	Lys	Ala 295	Leu	Glu	Ser	Ile	Lys 300	Val	Pro	Val	Leu
Val 305	Ala	Gly	Val	Asp	Thr 310	Asp	Ile	Leu	Tyr	Pro 315	Tyr	His	Gln	Gln	Glu 320
His	Leu	Ser	Arg	Asn 325	Leu	Gly	Asn	Leu 330	Leu	Ala	Met	Ala	Lys	Ile 335	Val
Ser	Pro	Val	Gly 340	His	Asp	Ala	Phe	Leu 345	Thr	Glu	Ser	Arg	Gln 350	Met	Asp
Arg	Ile 355	Val	Arg	Asn	Phe	Phe	Ser 360	Leu	Ile	Ser	Pro	Asp 365	Glu	Asp	Asn
Pro	Ser 370	Thr	Tyr	Ile	Glu	Phe	Tyr 375	Ile							

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<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA00403
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                                     Met Pro Thr Leu Ala
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Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	
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gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260
 gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275
 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290
 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305
 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325
 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340
 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355
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 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
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 <213> Corynebacterium glutamicum
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 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
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 Pro Ser
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<210> 181

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXC01207

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 Val Ser Arg Ile Tyr
 1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
 10 15 20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
 25 30 35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
 40 45 50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
 55 60 65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
 Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70 75 80 85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
 .90 95 100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
 105 110 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
 120 125 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
 135 140 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
 150 155 160 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu

200 205 210 771

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 Ser Leu Arg
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<210> 182
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160
 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190
 Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
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 Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 183
 <211> 1419
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1396)
 <223> RXC00152

<400> 183

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caaatagtagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
                                         Met Thr Gly Leu Ile
                                         1                               5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
                               10                               15                               20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
                               25                               30                               35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
                               40                               45                               50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
                               55                               60                               65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
                               70                               75                               80                               85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr
                               90                               95                               100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
                               105                               110                               115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
                               120                               125                               130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr
                               135                               140                               145

acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat 595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp
                               150                               155                               160                               165

ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac 643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp
                               170                               175                               180

cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc 691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala
                               185                               190                               195

gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct 739

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Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala
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gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa 787
 Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln
 215 220 225

gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag 835
 Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln
 230 235 240 245

gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag 883
 Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys
 250 255 260

tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag 931
 Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys
 265 270 275

ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca 979
 Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro
 280 285 290

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 Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala
 295 300 305

aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa
 1075
 Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu
 310 315 320 325

gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc
 1123
 Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser
 330 335 340

acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc
 1171
 Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val Ala Ala Asn Ala
 345 350 355

gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag
 1219
 Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys
 360 365 370

aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa
 1267
 Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln
 375 380 385

aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca
 1315
 Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala
 390 395 400 405

aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac
 1363
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr

410

415

420

tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg
1416

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425 430

cgg
1419

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<211> 432

<212> PRT

<213> Corynebacterium glutamicum

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Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
35 40 45

Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
50 55 60

Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
65 70 75 80

Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
85 90 95

Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
100 105 110

Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
115 120 125

Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
130 135 140

Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
145 150 155 160

Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
165 170 175

Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
180 185 190

Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
195 200 205

Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
210 215 220

Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
225 230 235 240



Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
 245 250 255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
 260 265 270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
 275 280 285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
 290 295 300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
 305 310 315 320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
 325 330 335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Val
 340 345 350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
 355 360 365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
 370 375 380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
 385 390 395 400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
 405 410 415

Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 420 425 430

<210> 185

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1147)

<223> RXA00115

<400> 185

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 Met Leu Asp Asn Ser
 1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
 10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	
25 30 35	
tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc	259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu	
40 45 50	
att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tcg gtc tcc cct gcc aac acg gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tcg atg tcc aag ttc ccg aat gtt cgc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr	
120 125 130	
gag ctc ttt gcc gtc gtt ggt ggt tcg atg ggt gcg cag caa acc tat	547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc	595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac	691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr	
185 190 195	
tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tcg cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
 265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
 280 285 290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca
 1027
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
 295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac
 1075
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
 310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa
 1123
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
 330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct
 1170
 Asn Leu Lys Glu Leu Phe Glu Ser
 345

<210> 186

<211> 349

<212> PRT

<213> *Corynebacterium glutamicum*

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Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
 35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
 50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
 65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
 85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
 100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
 115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
 130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
 210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
 225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
 245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
 260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
 275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
 290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
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<210> 187

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1231)

<223> RXN00403

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 Met Pro Thr Leu Ala
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cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
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gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
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cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
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ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc
 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

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 Glu Phe Tyr Ile
 375

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<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

85										90				95			
Gly	Pro	Gly	Ser	Met	His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe		
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Pro	Ala	Thr	Ser	Ile	Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu		
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Asp	Ala	Leu	Gly	Ile	Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met		
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Gly	Gly	Ala	Arg	Thr	Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val		
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Gly	Ala	Ala	Ala	Val	Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln		
				165					170					175			
Ile	Gly	Ile	Gln	Ser	Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His		
			180					185					190				
Trp	His	Glu	Gly	Asn	Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly		
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Leu	Gly	Ala	Ala	Arg	Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu		
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Glu	Ile	Asp	Glu	Arg	Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro		
225					230					235					240		
Leu	Gly	Pro	Tyr	Arg	Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr		
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Leu	Asp	Tyr	Gln	Ala	Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser		
			260					265					270				
Tyr	Val	Leu	Leu	Thr	Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp		
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Arg	Gly	Gly	Leu	Asn	Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu		
	290					295					300						
Val	Ala	Gly	Val	Asp	Thr	Asp	Ile	Leu	Tyr	Pro	Tyr	His	Gln	Gln	Glu		
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Ser	Pro	Val	Gly	His	Asp	Ala	Phe	Leu	Thr	Glu	Ser	Arg	Gln	Met	Asp		
			340					345					350				
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<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1210)

<223> FRXA00403

<400> 189

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Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                               10                               15                               20

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Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
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gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                               40                               45                               50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
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acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                               90                               95                               100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                               105                               110                               115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                               120                               125                               130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                               135                               140                               145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
                               150                               155                               160                               165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                               170                               175                               180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                               185                               190                               195

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tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
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cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

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 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
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 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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 Pro Ser
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 <223> RXS03158

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 Leu His Ser Thr Thr
 1 5
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80 85
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 90 95 100
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115
 gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
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 tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145
 cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595

His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
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gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
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 <213> Corynebacterium glutamicum

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 20 25 30

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 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
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<210> 193
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<222> (1) .. (594)

<223> FRXA00254

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1				5					10					15		
tac	atc	gga	gga	cac	tcc	gac	gtt	gtt	ggc	ggc	ctt	gtg	gtt	acc	aac	96
Tyr	Ile	Gly	Gly	His	Ser	Asp	Val	Val	Gly	Gly	Leu	Val	Val	Thr	Asn	
			20					25						30		
gac	cag	gaa	atg	gac	gaa	gaa	ctg	ctg	ttc	atg	cag	ggc	ggc	atc	gga	144
Asp	Gln	Glu	Met	Asp	Glu	Glu	Leu	Leu	Phe	Met	Gln	Gly	Gly	Ile	Gly	
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ccg	atc	cca	tca	gtt	ttc	gat	gca	tac	ctg	acc	gcc	cgt	ggc	ctc	aag	192
Pro	Ile	Pro	Ser	Val	Phe	Asp	Ala	Tyr	Leu	Thr	Ala	Arg	Gly	Leu	Lys	
	50					55					60					
acc	ctt	gca	gtg	cgc	atg	gat	cgc	cac	tgc	gac	aac	gca	gaa	aag	atc	240
Thr	Leu	Ala	Val	Arg	Met	Asp	Arg	His	Cys	Asp	Asn	Ala	Glu	Lys	Ile	
65					70					75					80	
gcg	gaa	ttc	ctg	gac	tcc	cgc	cca	gag	gtc	tcc	acc	gtg	ctc	tac	cca	288
Ala	Glu	Phe	Leu	Asp	Ser	Arg	Pro	Glu	Val	Ser	Thr	Val	Leu	Tyr	Pro	
				85					90					95		
ggt	ctg	aag	aac	cac	cca	ggc	cac	gaa	gtc	gca	gcg	aag	cag	atg	aag	336
Gly	Leu	Lys	Asn	His	Pro	Gly	His	Glu	Val	Ala	Ala	Lys	Gln	Met	Lys	
			100					105					110			
cgc	ttc	ggc	ggc	atg	atc	tcc	gtc	cgt	ttc	gca	ggc	ggc	gaa	gaa	gca	384
Arg	Phe	Gly	Gly	Met	Ile	Ser	Val	Arg	Phe	Ala	Gly	Gly	Glu	Glu	Ala	
		115					120					125				
gct	aag	aag	ttc	tgt	acc	tcc	acc	aaa	ctg	atc	tgt	ctg	gcc	gag	tcc	432
Ala	Lys	Lys	Phe	Cys	Thr	Ser	Thr	Lys	Leu	Ile	Cys	Leu	Ala	Glu	Ser	
	130					135					140					
ctc	ggt	ggc	gtg	gaa	tcc	ctc	ctg	gag	cac	cca	gca	acc	atg	acc	cac	480
Leu	Gly	Gly	Val	Glu	Ser	Leu	Leu	Glu	His	Pro	Ala	Thr	Met	Thr	His	
145					150					155					160	
cag	tca	gct	gcc	ggc	tct	cag	ctc	gag	gtt	ccc	cgc	gac	ctc	gtg	cgc	528
Gln	Ser	Ala	Ala	Gly	Ser	Gln	Leu	Glu	Val	Pro	Arg	Asp	Leu	Val	Arg	
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atc	tcc	att	ggt	att	gaa	gac	att	gaa	gac	ctg	ctc	gca	gat	gtc	gag	576
Ile	Ser	Ile	Gly	Ile	Glu	Asp	Ile	Glu	Asp	Leu	Leu	Ala	Asp	Val	Glu	
			180					185					190			
cag	gcc	ctc	aat	aac	ctt	tagaaactat	ttggcggcaa	gca								617
Gln	Ala	Leu	Asn	Asn	Leu											
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<212> PRT

<213> Corynebacterium glutamicum

<400> 194

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 35 40 45
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
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 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
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 Gln Ala Leu Asn Asn Leu
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<222> (101)..(1147)

<223> RXA02532

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 Met Asn Pro Pro Ile
 1 5
 acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163

Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu	Lys	Ala	Tyr	Gly	Arg	
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Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala	Ala	Met	Gly	Thr	Leu	
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Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Ala	Ala	Ala	Thr	
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Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr	Val	Val	Leu	Pro	Lys	
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Ala	Ala	Tyr	Tyr	Gly	Val	Thr	Asn	Ile	Phe	Ala	Arg	Met	Glu	Ala	Arg	
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gga	agg	ctg	aag	gtt	cga	act	gtt	gat	gca	gac	aat	acc	gaa	gaa	gtg	403
Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	Val	
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Ile	Ala	Ala	Ala	Gln	Gly	Ala	Asp	Val	Val	Trp	Val	Glu	Ser	Ile	Ala	
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Asn	Pro	Thr	Met	Val	Val	Ala	Asp	Ile	Pro	Ala	Ile	Val	Asp	Gly	Val	
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Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp	Ala	Thr	Phe	Ala	Thr	Pro	
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ctt	cgt	caa	cgt	cca	ttg	gaa	ctt	ggt	gct	gat	att	gtg	ctt	tac	tcg	595
Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp	Ile	Val	Leu	Tyr	Ser	
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gca	acc	aaa	ctt	atc	ggt	gga	cac	tct	gat	ctt	ctt	ctt	gga	gtc	gca	643
Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	Ala	
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gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	cat	691
Val	Cys	Lys	Ser	Glu	His	His	Ala	Gln	Phe	Leu	Ala	Thr	His	Arg	His	
			185					190					195			
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg	
		200					205					210				
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Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala	
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Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val	
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Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg	

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 Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala
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 aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc 979
 Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr
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 His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr
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 Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg
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 1123
 Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn
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 Ala Ser Ile Asp Lys Val Leu Gly
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<213> *Corynebacterium glutamicum*

<400> 196

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 35 40 45
 Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
 50 55 60
 Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
 65 70 75 80
 Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
 85 90 95
 Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
 100 105 110
 Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
 115 120 125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
 130 135 140
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
 145 150 155 160
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
 165 170 175
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
 180 185 190
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
 195 200 205
 Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210 215 220
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
 225 230 235 240
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
 245 250 255
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
 260 265 270
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
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 Leu Ser Phe Asp Pro
 1 5

 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163

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Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys	Gly	Tyr	Glu	Tyr	Thr	
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Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser	Ser	Gly	Met	Ala	Ala	
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Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg	Leu	Ile	Asp	Thr	Val	
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Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val	Asp	Thr	Ser	Val	Val	
		120					125					130				
gaa	gag	gtc	aag	gca	gcg	atc	aag	gac	aac	acc	aag	ctg	atc	tgg	gtg	547
Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr	Lys	Leu	Ile	Trp	Val	
	135					140					145					
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Glu	Thr	Pro	Thr	Asn	Pro	Ala	Leu	Gly	Ile	Thr	Asp	Ile	Glu	Ala	Val	
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Ala	Lys	Leu	Thr	Glu	Gly	Thr	Asn	Ala	Lys	Leu	Val	Val	Asp	Asn	Thr	
				170				175						180		
ttg	gca	tcc	cca	tac	ctg	cag	cag	cca	cta	aaa	ctc	ggc	gca	cac	gca	691
Leu	Ala	Ser	Pro	Tyr	Leu	Gln	Gln	Pro	Leu	Lys	Leu	Gly	Ala	His	Ala	
			185					190					195			
agt	cct	tgc	act	cca	cca	cca	agt	aca	tcg	aag	gac	act	ccg	acg	ttg	739
Ser	Pro	Cys	Thr	Pro	Pro	Pro	Ser	Thr	Ser	Lys	Asp	Thr	Pro	Thr	Leu	
		200					205					210				
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Leu	Ala	Ala	Leu	Trp	Val	Pro	Thr	Thr	Arg	Lys	Trp	Thr	Lys	Asn	Cys	
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Cys	Ser	Cys	Arg	Ala	Ala	Ser	Asp	Arg	Ser	His	Gln	Phe	Ser	Met	His	
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Thr																

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 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140
 Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
 145 150 155 160
 Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
 165 170 175
 Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
 180 185 190
 Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys
 195 200 205
 Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
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 Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
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 Gln Phe Ser Met His Thr
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<222> (101)..(703)

<223> FRXA02768

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aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
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gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
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ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
                                   40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
                                   55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
                                   70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                                   90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
                                   105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
                                   120 125 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
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gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
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gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
                                   170 175 180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
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703

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Xaa His Thr Gln
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<212> PRT
<213> Corynebacterium glutamicum

<400> 200

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35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
130 135 140

Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
145 150 155 160

Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
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Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
180 185 190

Pro Leu Lys Xaa Xaa Xaa His Thr Gln
195 200

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                                Leu Gly Ala Tyr Gly
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tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
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cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
                                25                                30                                35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
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atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
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Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
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Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
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Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
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Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
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Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
                                150                                155                                160                                165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                                170                                175                                180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
                                185                                190                                195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
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 230 235 240 245
 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
 250 255 260
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 265 270 275
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 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
 280 285 290
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 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag
 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325
 gat tca tgc gac ctt taaggcttta ccggcgctgg gtg
 1113
 Asp Ser Cys Asp Leu
 330

<210> 202
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 202
 Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
 305 310 315 320
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
 325 330

<210> 203

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 203

act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15

gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala

20	25	30	
ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc			144
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr			
35	40	45	
ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt			192
Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu			
50	55	60	
tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa			240
Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu			
65	70	75	80
ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg			288
Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu			
85	90	95	
aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac			336
Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr			
100	105	110	
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct			384
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala			
115	120	125	
tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc			432
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile			
130	135	140	
ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca			480
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser			
145	150	155	160
cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc			528
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr			
165	170	175	
gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac			576
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp			
180	185	190	
ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca			623
Leu Glu Gly Gly Phe Ala Ala Ile			
195	200		

<210> 204

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Thr	Asp	Glu	Lys	Asp	Gly	Lys	Pro	Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro
1					5				10					15	

Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala
			20					25					30		

Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr
		35					40					45			

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 205

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 205

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 1 5 10 15
 tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30
 ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45
 gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60
 gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val

65	70	75	80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc				288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag				336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag				384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	115	120	125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt				432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	130	135	140	
cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca				480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala	145	150	155	160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag				528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu	165	170	175	
acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc				576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile	180	185	190	
tagcttttaa tagactcacc cca				599
<210> 206				
<211> 192				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 206				
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys				
1 5 10 15				
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly				
20 25 30				
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala				
35 40 45				
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn				
50 55 60				
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val				
65 70 75 80				
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr				
85 90 95				
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu				
100 105 110				
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys				

115	120	125
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val		
130	135	140
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala		
145	150	155
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu		
	165	170
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile		
	180	185
		190

<210> 207

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXA00405

<400> 207

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ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
                                         Met Pro Lys Tyr Asp
                                         1           5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
              10              15              20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
              25              30              35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
              40              45              50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
              55              60              65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
              70              75              80              85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
              90              95              100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu

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	105	110	115	
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt				499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly				
	120	125	130	
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag				547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln				
	135	140	145	
gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc				595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala				
	150	155	160	165
aac cca cag gca gac gtc				613
Asn Pro Gln Ala Asp Val				
	170			

<210> 208

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr				
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Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg				
20 25 30				
Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu				
35 40 45				
His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser				
50 55 60				
Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser				
65 70 75 80				
Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala				
85 90 95				
Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val				
100 105 110				
Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr				
115 120 125				
Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp				
130 135 140				
Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe				
145 150 155 160				
Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val				
165 170				

<210> 209

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXA02197

<400> 209

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Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1                               5                               10                               15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac      96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
                               20                               25                               30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct      144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
                               35                               40                               45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag      192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
                               50                               55                               60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc      240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
   65                               70                               75                               80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt      288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
                               85                               90                               95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac      336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
                               100                              105                              110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct      384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
                               115                              120                              125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt      432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
                               130                              135                              140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc      480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
                               145                              150                              155                              160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc      528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
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taacaccttt gagaggaaa act                                          551

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<210> 210

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

<210> 211

<211> 2599

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2599)

<223> RXN02198

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agttcgggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca .gtt 115
 Met Ser Thr Ser Val
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu

25	30	35	
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg			259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly			
40	45	50	
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att			307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile			
55	60	65	
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act			355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr			
70	75	80	85
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt			403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg			
90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct			451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala			
105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt			499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly			
120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat			547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr			
135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac			595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp			
150	155	160	165
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag			643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln			
170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat			691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Leu Asp			
185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc			739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr			
200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca			787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro			
215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag			835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu			
230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg			883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val			
250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca			931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala			
265	270	275	

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gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe
      280                      285                      290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca
1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr
      295                      300                      305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag
1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
310                      315                      320                      325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
      330                      335                      340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
      345                      350                      355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
      360                      365                      370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
      375                      380                      385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390                      395                      400                      405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
      410                      415                      420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
      425                      430                      435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
      440                      445                      450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
      455                      460                      465

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ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
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 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
 1603
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
 490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
 1651
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
 505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
 1699
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
 1747
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
 1795
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
 550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
 1843
 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
 570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
 1891
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 1939
 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
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 1987
 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
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 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
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 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
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 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
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 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
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<212> PRT

<213> Corynebacterium glutamicum

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Val	Leu	Arg	Gln	Ile	His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu
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Val	Glu	Thr	Asn	Thr	Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr
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Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val
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 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
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 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
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 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
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 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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655

Asp

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Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
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ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211

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His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr		
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Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp		
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 745 750 755

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Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val
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 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys



645

650

655

Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

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Ser Gly Leu Leu Val Lys Ser Thr Val Val
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<222> (101) .. (598)

<223> RXN03074

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Met Thr Gln Ser Ala
1 5

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cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac    163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
          10                      15                      20

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Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tgc att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

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Glu Ala Pro Ile Lys Gln
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 Met Thr Gln Ser Ala
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cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
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gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
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<400> 218

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 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

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Glu Ala Pro Ile Lys Gln
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<210> 219

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<223> RXN00132

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Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	Ala	Gly	Arg	His	Gln	
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Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys	
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gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggg	tct	259
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser	
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Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala	
		55				60					65					

ttg	ggc	gct	gag	gtt	cgt	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln	
	70				75					80					85	

gat	gag	gct	gca	gcg	gct	atc	gtt	gtc	ggc	tcc	ggc	acc	gtc	gaa	gag	403
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu	
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cca	gct	ggg	gtt	cca	gta	ttc	gcg	tgg	aag	ggg	gag	tca	ctg	gag	gag	451
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu	
			105					110					115			

tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca	499
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro	
		120					125					130				

aac	atg	atc	ctc	gac	gac	ggc	ggg	gac	gcc	acc	atg	gct	gtt	att	cgc	547
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg	
		135				140					145					

ggg	cgc	gaa	tac	gag	cag	gct	ggg	ctg	gtt	cca	cca	gca	gag	gcc	aac	595
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn	
	150				155					160					165	

gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt	643
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu	
			170						175					180		

gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggg	691
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly	
			185					190						195		

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val
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acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
 1027
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
 1075
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg
 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg
 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag
 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc
 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc
 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac
 1363



Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420
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 1411
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
 425 430 435
 gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc
 1459
 Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
 440 445 450
 gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc
 1507
 Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
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 20 25 30
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 35 40 45
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145		150		155		160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met						
		165		170		175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala						
		180		185		190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg						
		195		200		205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn						
		210		215		220
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr						
		225		230		235
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met						
		245		250		255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly						
		260		265		270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu						
		275		280		285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val						
		290		295		300
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala						
		305		310		315
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys						
		325		330		335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp						
		340		345		350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys						
		355		360		365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val						
		370		375		380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro						
		385		390		395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile						
		405		410		415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu						
		420		425		430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu						
		435		440		445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly						
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 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
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 Tyr Arg Tyr
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 Tyr Arg Tyr
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 Met Ala Gln Val Met
 1 5
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

10						15						20						
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Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys			
			25					30					35					
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggc	tct	259		
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser			
		40					45					50						
atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct	307		
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala			
		55				60					65							
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	70				75					80					85			
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Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu			
				90					95					100				
cca	gct	ggc	gtt	cca	gta	ttc	gcg	tgg	aag	ggc	gag	tca	ctg	gag	gag	451		
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu			
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Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro			
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aac	atg	atc	ctc	gac	gac	ggc	ggc	gac	gcc	acc	atg	gct	gtt	att	cgc	547		
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg			
	135					140					145							
ggc	cgc	gaa	tac	gag	cag	gct	ggc	ctg	gtt	cca	cca	gca	gag	gcc	aac	595		
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn			
	150				155					160					165			
gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt	643		
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu			
			170						175					180				
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggc	691		
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly			
			185					190					195					
gtc	acc	gag	gaa	acc	acc	acc	ggc	gtg	cac	cgc	ctg	tac	cac	ttc	gct	739		
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala			
		200					205					210						
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc	787		
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val			
	215					220					225							
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835		
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile			
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Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val			
			250						255					260				

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Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
310 315 320 325

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1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg
1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag
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His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
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1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
375 380 385

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1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac
1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
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Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys



325

330

335

Asp	His	Ala	Leu	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp
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Met	His	Ser	Leu	Leu	His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys
		355					360					365			
Pro	Gln	Val	Asp	Glu	Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val
	370					375					380				
Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro
385					390					395					400
Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile
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Glu	Leu	Phe	Gln	Asn	Glu	Gly	Gln	Tyr	Glu	Asn	Glu	Val	Tyr	Arg	Leu
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<223> RXN02085
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Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
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aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggT	cgc	gaa	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
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Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	
		40					45					50				
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Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	
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atg	ctc	gat	acc	gcc	gct	att	ttg	ggT	gtg	ctg	ccg	gag	cgt	ttt	gat	355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	
70					75				80					85		

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
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 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

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 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

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 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
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 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
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 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
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 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
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cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
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cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

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 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
 585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc
 1939
 Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
 600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg
 1987
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 615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat
 2035
 Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
 630 635 640 645

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 2083
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
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 2131
 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
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 2179
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
 680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
 2227
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
 695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
 2275
 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
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 2323
 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
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 Gly Ala Thr Ile
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 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
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 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
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 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
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 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr

530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
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 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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 740 745

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1900)
 <223> FRXA02085

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 Met Thr Ser Asn Phe
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 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu

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Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu														
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Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg														
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tac	ttt	ggc	gct	gct	cgc	ggc	act	gag	acc	ctg	cct	gca	cag	gca	atg														
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met														
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acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct														
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser														
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cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggc	tcc	aac	cct														
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro														
				170					175					180															
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Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys														
			185					190					195																
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gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggc	tac	acc	act														
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr														
			215			220					225																		
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Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly														
					235					240				245															
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc														
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly														
				250					255					260															

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tgc gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595
 aga cgt cga taagcctgcc tacctgcagt ggt
 1923
 Arg Arg Arg
 600

<210> 228

<211> 600

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 228

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 1 5 10 15
 Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355					360					365								
Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro			
370					375					380								
Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg			
385					390					395					400			
Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr			
					405					410					415			
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala			
					420					425					430			
Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met			
					435					440					445			
Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu			
					450					455					460			
Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr			
					465					470					475		480	
Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val			
					485					490					495			
Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn			
					500					505					510			
Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln			
					515					520					525			
Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr			
					530					535					540			
Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr			
					545					550					555		560	
Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile			
					565					570					575			
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu			
					580					585					590			
Leu	Leu	Pro	Ala	Thr	Arg	Arg	Arg											
					595					600								

<210> 229

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 229

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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
                               Met Ser Leu Arg Phe
                               1                               5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
                               10                               15                               20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
                               25                               30                               35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
                               40                               45                               50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
                               55                               60                               65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
                               70                               75                               80                               85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
                               90                               95                               100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
                               105                               110                               115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
                               120                               125                               130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
                               135                               140                               145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150                               155                               160

aac 603

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<210> 230

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
 1                               5                               10                               15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
                20                               25                               30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35                               40                               45

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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 231
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 231
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403			
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
90 95 100				
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat	451			
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
105 110 115				
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499			
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
120 125 130				
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547			
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
135 140 145				
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595			
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
150 155 160 165				
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643			
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
170 175 180				
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691			
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
185 190 195				
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739			
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
200 205 210				
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg	787			
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
215 220 225				
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835			
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
230 235 240 245				
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883			
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
250 255 260				
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931			
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
265 270 275				
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979			
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
280 285 290				
ggg gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
295 300 305				
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325
 cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340
 gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355
 aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370
 ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385
 gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400
 aacgagggtt gct
 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125



Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 233

<211> 548

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 233

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20             25             30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35             40             45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
  50             55             60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
  65             70             75             80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85             90             95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100             105             110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115             120             125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130             135             140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145             150             155             160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165             170             175

taagctagac aacgagggtt gct 548

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<210> 234

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

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Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile
			20					25					30		
Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile
		35					40					45			
Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly
	50					55					60				
Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe
	65				70					75					80
Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu
				85					90					95	
Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His
			100					105					110		
Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val
		115					120					125			
Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp
	130					135					140				
Cys	Gly	Leu	Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	Lys	Leu
	145				150					155					160
Glu	Ser	Leu	Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu	Phe	
				165					170					175	

<210> 235
<211> 784
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> FRXA02658

<400> 235
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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 236

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

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 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu

50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 237
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

<400> 237
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 ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser 1 5
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 25 30 35

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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
      40                      45                      50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                      60                      65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70                      75                      80                      85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90                      95

cac 408

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<210> 238
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

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<400> 238
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
      20                      25                      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
      35                      40                      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
      50                      55                      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
      65                      70                      75                      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      85                      90                      95

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<210> 239
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1804)
<223> RXC00128

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
                        Val Ser Lys Ile Ser
                        1                      5

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acg	aaa	ctg	aag	gcc	ctc	acc	gcg	gtg	ctg	tct	gtg	acc	act	ctg	gtg	163
Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser	Val	Thr	Thr	Leu	Val	
				10					15					20		
gct	ggg	tgt	tcc	acg	ctt	ccg	cag	aac	acg	gat	ccg	caa	gtg	ctg	cgc	211
Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp	Pro	Gln	Val	Leu	Arg	
			25					30					35			
tca	ttt	tcc	ggg	tcc	caa	agc	aca	caa	gag	ata	gca	ggg	ccg	acc	ccg	259
Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile	Ala	Gly	Pro	Thr	Pro	
		40					45					50				
aat	caa	gat	ccg	gat	ttg	ttg	atc	cgc	ggc	ttc	ttc	agc	gca	ggg	gcg	307
Asn	Gln	Asp	Pro	Asp	Leu	Leu	Ile	Arg	Gly	Phe	Phe	Ser	Ala	Gly	Ala	
	55				60						65					
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Tyr	Pro	Thr	Gln	Gln	Tyr	Glu	Ala	Ala	Lys	Ala	Tyr	Leu	Thr	Glu	Gly	
	70				75					80					85	
acg	cgc	agc	acg	tgg	aat	ccg	gct	gcg	tcg	act	cgt	att	ttg	gat	cgc	403
Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr	Arg	Ile	Leu	Asp	Arg	
				90					95					100		
att	gat	ctg	aac	act	ctg	cca	ggg	tcg	acg	aat	gcg	gaa	cga	acg	att	451
Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn	Ala	Glu	Arg	Thr	Ile	
			105					110					115			
gcg	atc	cgt	gga	acg	cag	gtc	gga	acg	ttg	ctc	agc	ggg	ggc	gtg	tat	499
Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu	Ser	Gly	Gly	Val	Tyr	
		120					125					130				
cag	ccg	gag	aat	gcg	gag	ttt	gaa	gct	gag	atc	acg	atg	cgt	cgg	gaa	547
Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile	Thr	Met	Arg	Arg	Glu	
	135					140					145					
gat	ggg	gag	tgg	cgt	atc	gat	gct	ttg	ccg	gac	ggg	att	tta	tta	gag	595
Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp	Gly	Ile	Leu	Leu	Glu	
	150				155					160					165	
aga	aac	gat	ctg	cgg	aac	cat	tac	act	ccg	cac	gat	gtg	tat	ttc	ttt	643
Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His	Asp	Val	Tyr	Phe	Phe	
				170					175					180		
gat	cct	tct	ggc	cag	gtg	ttg	gtg	ggg	gat	cgg	cgt	tgg	ttg	ttc	aat	691
Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg	Arg	Trp	Leu	Phe	Asn	
			185					190					195			
gag	tcg	cag	tcg	atg	tcc	acg	gtg	ctg	atg	gcc	ctt	ctg	ggt	aat	ggg	739
Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	Leu	Leu	Val	Asn	Gly	
		200					205					210				
cct	tcg	ccg	gca	att	tct	cct	ggg	gtg	gtc	aat	cag	ctg	tcc	acg	gat	787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp	
	215					220					225					
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggg	ttg	835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu	
	230				235					240					245	
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg	883

Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg
 1027
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
 295 300 305

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 1075
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
 310 315 320 325

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 1123
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
 330 335 340

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 1171
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
 1219
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
 1267
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
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 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
 1459
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
 1507
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465

 gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
 1555
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485

 gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
 1603
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500

 cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
 1651
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515

 ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530

 gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
 1747
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
 535 540 545

 att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
 1795
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
 550 555 560 565

 gtt gcg tac tgatggagct gttcttcccg cgc
 1827
 Val Ala Tyr

<210> 240
 <211> 568
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 240
 Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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 Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
 20 25 30

 Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45

 Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60

 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80



Tyr	Leu	Thr	Glu	Gly	Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr	85	90	95
Arg	Ile	Leu	Asp	Arg	Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn	100	105	110
Ala	Glu	Arg	Thr	Ile	Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu	115	120	125
Ser	Gly	Gly	Val	Tyr	Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile	130	135	140
Thr	Met	Arg	Arg	Glu	Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp	145	150	155
Gly	Ile	Leu	Leu	Glu	Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His	165	170	175
Asp	Val	Tyr	Phe	Phe	Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg	180	185	190
Arg	Trp	Leu	Phe	Asn	Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	195	200	205
Leu	Leu	Val	Asn	Gly	Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	210	215	220
Gln	Leu	Ser	Thr	Asp	Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	225	230	235
Gln	Phe	Thr	Gly	Leu	Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	245	250	255
Ala	Ala	Gln	Ala	Val	Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	260	265	270
Tyr	Thr	Leu	Val	Ala	Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	275	280	285
Leu	Thr	Thr	Asp	Asp	Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	290	295	300
Thr	Val	Ser	Thr	Leu	Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	305	310	315
Ser	Ser	Gly	Asn	Val	Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	325	330	335
Ile	Asp	Ser	Ala	Ala	Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	340	345	350
Arg	His	Glu	Asn	Asn	Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	355	360	365
Val	Thr	Ser	Asp	Ala	Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	370	375	380
Glu	Tyr	Ala	Ser	Ser	Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	385	390	395

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
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Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
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<210> 241
 <211> 1344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1321)
 <223> RXA02240

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 aagactattt attctcaact tcttcgaaaag aagggtattt gtg gct cag cca acc 115
 Val Ala Gln Pro Thr
 1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
 10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
 25 30 35

aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile 55 60 65			307
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc
 1027
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
 295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca
 1075
 Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
 310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc
 1123
 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
 330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg
 1171
 Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
 345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac
 1219
 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
 360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt
 1267
 Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
 375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag
 1315
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
 390 395 400 405

ttg gcc taaaaatctg atgtagtacc ttc
 1344
 Leu Ala

<210> 242

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
 1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
 20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
 35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
 50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65	70					75					80				
Gly	Phe	Asn	Ser	Ser	Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val
				85					90					95	
Ser	Val	Ser	Ile	Gly	Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp
			100					105					110		
Asn	Ser	Asp	Glu	Ala	Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg
		115						120				125			
Ala	Gly	Ala	Gly	Asp	Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu
	130					135					140				
Thr	Glu	Glu	Tyr	Met	Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser
145					150					155					160
Arg	Arg	Leu	Thr	Gln	Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg
				165					170					175	
Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg
			180					185					190		
Pro	Ser	His	Leu	Asp	Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu
		195					200					205			
Val	Asp	Arg	Ala	Trp	Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp
	210					215					220				
Trp	Val	Ile	Lys	Asp	Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile
225					230					235					240
Thr	Val	Leu	Ile	Asn	Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met
				245					250					255	
Gly	Asp	Ala	Gly	Leu	Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly
			260					265					270		
Gly	Met	Ala	Arg	His	Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser
		275					280					285			
Lys	Val	Asp	Arg	Ser	Ala	Ala	Tyr	Ala	Met	Arg	Trp	Val	Ala	Lys	Asn
	290					295					300				
Ile	Val	Ala	Ala	Gly	Leu	Ala	Asp	Arg	Ala	Glu	Val	Gln	Val	Ala	Tyr
305					310					315					320
Ala	Ile	Gly	Arg	Ala	Lys	Pro	Val	Gly	Leu	Tyr	Val	Glu	Thr	Phe	Asp
				325					330					335	
Thr	Asn	Lys	Glu	Gly	Leu	Ser	Asp	Glu	Gln	Ile	Gln	Ala	Ala	Val	Leu
			340					345						350	
Glu	Val	Phe	Asp	Leu	Arg	Pro	Ala	Ala	Ile	Ile	Arg	Glu	Leu	Asp	Leu
		355					360					365			
Leu	Arg	Pro	Ile	Tyr	Ala	Asp	Thr	Ala	Ala	Tyr	Gly	His	Phe	Gly	Arg
	370					375					380				
Thr	Asp	Leu	Asp	Leu	Pro	Trp	Glu	Ala	Ile	Asp	Arg	Val	Asp	Glu	Leu
385					390					395					400

Arg Ala Ala Leu Lys Leu Ala
405

<210> 243
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA00780

<400> 243
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tcacgctgtt agacttgcct gcatgctctc gacaataaaa atg atc cgt gaa gat 115
Met Ile Arg Glu Asp
1 5
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
10 15 20
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
25 30 35
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
40 45 50
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
55 60 65
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
70 75 80 85
ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
90 95 100
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc eac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
105 110 115
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
120 125 130
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
135 140 145
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
 170 175 180

att taagaacagt tagcgcccta cct 669
 Ile

<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala
 1 5 10 15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
 20 25 30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
 35 40 45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
 50 55 60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
 65 70 75 80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
 85 90 95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
 100 105 110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
 115 120 125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
 130 135 140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
 145 150 155 160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
 165 170 175

Asp Pro Asp Tyr Tyr Ile
 180

<210> 245

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)


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ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787
Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile
215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835
Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser
230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883
Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly
250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc
1027
Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
295 300 305

cgc gac taattcttag cgactgttaa cca
1056
Arg Asp
310

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<210> 246

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

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Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
115 120 125

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Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser
 195 200 205
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
 210 215 220
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
 225 230 235 240
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu
 245 250 255
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile
 260 265 270
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr
 275 280 285
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val
 290 295 300
 Leu Tyr Glu Asp Ile Arg Asp
 305 310

<210> 247

<211> 623

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 247

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 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80
 ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 248

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 248

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80



Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	
				85					90							
Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	
				100					105							
Thr	Gly	Ser	Val	Leu	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala	
				115					120							
Trp	Ala	Phe	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Ile	
				130					135							
Gly	Asp	Val	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser	
145					150					155						
Gln	Ser	Asp	Glu	Ala	Gly	Leu	Ala	Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	
				165					170							
Val	Arg	Leu	Ser	Val	Gly	Ile	Glu	Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp	
				180					185							
Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile									
				195					200							

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<210> 249
<211> 599
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(576)  
<223> FRXA00402
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<400> 249																
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Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	
1				5					10					15		
tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	96
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	
			20					25					30			
ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tgg	gct	144
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	
		35					40					-45				
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac	192
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	
	50					55					60					
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	240
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val	
65					70					75					80	
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tgg	tac	gca	acc	288
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	
				85					90					95		
aag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag	336

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190
 tagctttaaa tagactcacc cca 599

<210> 250

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
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 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190

<210> 251
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(613)
 <223> RXS00405

<400> 251
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 ggagaagaat ttctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
 Met Pro Lys Tyr Asp
 1 5
 aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
 10 15 20
 ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
 25 30 35
 caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
 40 45 50
 ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
 55 60 65
 acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
 70 75 80 85
 cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
 90 95 100
 ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
 105 110 115
 tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
 Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
 120 125 130
 atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145
 gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165
 aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
 170

<210> 252
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 252
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 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
 165 170

<210> 253
 <211> 1812
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1789)
 <223> RXC00164



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ggccagcctg cgcgaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115
Val Gly Arg Ile Pro
1 5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
10 15 20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
55 60 65

ttc	tat	gtg	gtg	tcg	cgg	att	tct	gag	aag	att	atc	gcc	aat	ttg	agg	355
Phe	Tyr	Val	Val	Ser	Arg	Ile	Ser	Glu	Lys	Ile	Ile	Ala	Asn	Leu	Arg	
70					75					80					85	

gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403
Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu
90 95 100

gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451
Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser
105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499
Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser
120 125 130

ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547
Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp
135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595
Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala
150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643
Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg
170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691
Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly
185 190 195

cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739
 Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln
 200 205 210

att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787

Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg
 215 220 225
 acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc 835
 Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu
 230 235 240 245
 atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat 883
 Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn
 250 255 260
 gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt 931
 Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg
 265 270 275
 ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa 979
 Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln
 280 285 290
 tcc ggc tat gcg tcg ctg gcg cgc atc gtg gga gtt gtt gcg gat ccg
 1027
 Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro
 295 300 305
 ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg
 1075
 Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val
 310 315 320 325
 gaa ttg cgc aac gtc agc ttt agc tat ggc gat tcc tgg gcg gtg aaa
 1123
 Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys
 330 335 340
 gac atc gac atc acg atc aat tcc ggc gaa act gtc gcg ctc gtg ggc
 1171
 Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly
 345 350 355
 gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg
 1219
 Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu
 360 365 370
 cgg gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct
 1267
 Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser
 375 380 385
 cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag
 1315
 His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln
 390 395 400 405
 gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct
 1363
 Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala
 410 415 420
 aaa cca gat gcc tcc gat gag gaa tta gcg cat gct ctt ggg caa gtt
 1411

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val
 425 430 435
 aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc
 1459
 Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val
 440 445 450
 gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg
 1507
 Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu
 455 460 465
 gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat
 1555
 Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp
 470 475 480 485
 gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag
 1603
 Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu
 490 495 500
 gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac
 1651
 Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His
 505 510 515
 cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag
 1699
 Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530
 ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg
 1747
 Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545
 ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga
 1789
 Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
 550 555 560
 tagttgactg ttcaatgcgt tga
 1812

<210> 254

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

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 Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu
 20 25 30
 Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys
 210 215 220
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu
 225 230 235 240
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys
 245 250 255
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val
 260 265 270
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val
 275 280 285
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly
 290 295 300
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala
 305 310 315 320
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp
 325 330 335
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr
 340 345 350
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp
 370 375 380
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu
 385 390 395 400
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln
 405 410 415
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His
 420 425 430
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu
 435 440 445
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val
 450 455 460
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala
 465 470 475 480
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala
 485 490 495
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala
 500 505 510
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile
 515 520 525
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu
 530 535 540
 Leu Leu Asp His Gly Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser
 545 550 555 560
 Val Gly Arg

<210> 255
 <211> 1713
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1690)
 <223> RXC01191

<400> 255
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 cgtgttggtg gccgtcgcgg ggttggtagg gccctgggcg gtg ggt gga ctc gtc 115
 Val Gly Gly Leu Val
 1 5
 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
 10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag cgg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
150 155 160 165	
ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931

Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala
 265 270 275

gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala
 280 285 290

tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc
 1027
 Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile
 295 300 305

aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg
 1075
 Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val
 310 315 320 325

ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc
 1123
 Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly
 330 335 340

ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt
 1171
 Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe
 345 350 355

tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc
 1219
 Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser
 360 365 370

caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc
 1267
 Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile
 375 380 385

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat
 1315
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp
 390 395 400 405

att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc
 1363
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile
 410 415 420

gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg
 1411
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met
 425 430 435

gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat
 1459
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp
 440 445 450

gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat
 1507
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp
 455 460 465

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
520 525 530

cccaagacca cgc
1713

<210> 256

<211> 530

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 256

Val Gly Gly Leu Val Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp
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Val Val Val Phe Ala Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser
20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro
35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu
 165 170 175
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp
 180 185 190
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn
 195 200 205
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe
 210 215 220
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala
 225 230 235 240
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly
 245 250 255
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val
 260 265 270
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala
 275 280 285
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His
 290 295 300
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu
 305 310 315 320
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala
 325 330 335
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu
 340 345 350
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys
 355 360 365
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu
 370 375 380
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His
 385 390 395 400
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln
 405 410 415
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile



485 490 495
 Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
 500 505 510
 Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
 515 520 525
 Ala Arg
 530

 <210> 257
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXA02646

 <400> 257
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 catgagtgaacacatacgtgt ctgagaaaag tccaggagtg atg gct agc gga gcg 115
 Met Ala Ser Gly Ala
 1 5
 gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
 Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
 10 15 20
 tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
 Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
 25 30 35
 gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
 Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
 40 45 50
 cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
 Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
 55 60 65
 caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
 Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His
 70 75 80 85
 gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc 403
 Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg
 90 95 100
 atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg 451
 Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met
 105 110 115
 gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc 499
 Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe
 120 125 130

gac gaa gca tgc gct gca gcg cat gaa gat gca gag cgc acc ggc gca 547
 Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala
 135 140 145

acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc 595
 Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly
 150 155 160 165

acc gtg gct gct gag atc ttg tgc cag ctg act tcc atg ggc aag agt 643
 Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser
 170 175 180

gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt 691
 Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly
 185 190 195

gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt 739
 Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly
 200 205 210

atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt 787
 Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly
 215 220 225

gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca 835
 Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala
 230 235 240 245

gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag 883
 Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln
 250 255 260

ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag 931
 Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu
 265 270 275

atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc 979
 Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly
 280 285 290

gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct
 1027
 Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser
 295 300 305

gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat
 1075
 Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr
 310 315 320 325

gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac
 1123
 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg
 1171
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu
 345 350 355

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc
 1219
 Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
 360 365 370

 aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg
 1267
 Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
 375 380 385

 agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg
 1315
 Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
 390 395 400 405

 gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac
 1363
 Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
 410 415 420

 ttg acc taaacatagc tgaaggccac ctc
 1392
 Leu Thr

<210> 258
 <211> 423
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
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 20 25 30

 Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
 35 40 45

 Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
 50 55 60

 Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
 65 70 75 80

 Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
 85 90 95

 Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
 100 105 110

 Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
 115 120 125

 Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala
 130 135 140

 Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr
 145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr
 165 170 175
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly
 180 185 190
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg
 195 200 205
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala
 210 215 220
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe
 225 230 235 240
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile
 245 250 255
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly
 260 265 270
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile
 275 280 285
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser
 290 295 300
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn
 305 310 315 320
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg
 325 330 335
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln
 340 345 350
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr
 355 360 365
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu
 370 375 380
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu
 385 390 395 400
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr
 405 410 415
 Pro Glu Tyr Glu Tyr Leu Thr
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<210> 259

<211> 966

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (943)

<223> RXA00766

<400> 259

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Met Val Phe Trp Asp
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln
200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
 215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu
 230 235 240 245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His
 250 255 260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
 265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
 Lys Ala Leu Gly
 280

<210> 260
 <211> 281
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 260

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Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His
 20 25 30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
 35 40 45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
 50 55 60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
 65 70 75 80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
 85 90 95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
 100 105 110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
 115 120 125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
 130 135 140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
 145 150 155 160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser



180										185					190				
Phe	Lys	Gly	Asp	Lys	Ile	Arg	Thr	Pro	Ser	Pro	Gly	Gly	Asp	Ile	Leu				
		195					200					205							
Pro	Gly	Thr	Thr	Gln	Ala	Ala	Leu	Phe	Ala	His	Ala	Thr	Glu	Lys	Gly				
	210					215					220								
Trp	Arg	Cys	Lys	Glu	Lys	Asp	Leu	Ser	Ile	Asp	Asp	Leu	Phe	Gly	Ala				
225					230					235					240				
Asp	Ser	Val	Trp	Leu	Val	Ser	Ser	Val	Arg	Gly	Pro	Val	Arg	Val	Thr				
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Arg	Leu	Asp	Gly	His	Lys	Leu	Arg	Lys	Pro	Asp	Asn	Glu	Lys	Glu	Ile				
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Lys	Ala	Leu	Ile	Thr	Lys	Ala	Leu	Gly											
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<210> 261

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXN01690

<400> 261

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actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 115
Met Thr Ser Leu Glu
1 5
ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
10 15 20
gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
25 30 35
gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259
Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
40 45 50
gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
55 60 65
tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
70 75 80 85
gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 403
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln
90 95 100

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cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt 451
 Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe
 105 110 115

att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct 499
 Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro
 120 125 130

gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc 547
 Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser
 135 140 145

acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg 595
 Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu
 150 155 160 165

gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct 643
 Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro
 170 175 180

gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga 691
 Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly
 185 190 195

act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc 739
 Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala
 200 205 210

cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat 787
 Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Trp Leu Asp
 215 220 225

gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg 835
 Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly
 230 235 240 245

ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt 883
 Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu
 250 255 260

tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta 931
 Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val
 265 270 275

gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc 979
 Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr
 280 285 290

gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct
 1027
 Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala
 295 300 305

tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct
 1075
 Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala
 310 315 320 325

cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg
 1123

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc
 1224

<210> 262
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 262

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 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 355 360 365

<210> 263
 <211> 1076
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1053)
 <223> FRXA01690

<400> 263

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ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg	96
Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
20 25 30	
cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc	144
His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
35 40 45	
acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc	192
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
50 55 60	
tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac	240
Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	

65	70					75					80					
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg	85					90					95					288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu																
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat	100					105					110					336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp																
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc	115					120					125					384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg																
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat	130					135					140					432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp																
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc	145					150					155					480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr																
ggg gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc	165					170					175					528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg																
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg	180					185					190					576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala																
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag	195					200					205					624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln																
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt	210					215					220					672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly																
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta	225					230					235					720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu																
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag	245					250					255					768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys																
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga	260					265					270					816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg																
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg	275					280					285					864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met																
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc	290					295					300					912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly																
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc	305					310					315					960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val																

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa
 1008
 Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc
 1053
 Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 340 345 350

taaatcaacc gggtttaaga ccc
 1076

<210> 264
 <211> 351
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
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 Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 20 25 30
 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 35 40 45
 Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 50 55 60
 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 65 70 75 80
 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 85 90 95
 Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 100 105 110
 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 115 120 125
 Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 130 135 140 -
 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 145 150 155 160
 Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 165 170 175
 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 180 185 190
 Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 195 200 205
 Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

210	215	220
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu		
225	230	235 240
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys		
	245	250 255
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg		
	260	265 270
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met		
	275	280 285
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly		
	290	295 300
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val		
	305	310 315 320
Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln		
	325	330 335
Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly		
	340	345 350

<210> 265

<211> 1782

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1759)

<223> RXN01026

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tatagtgaga tttacagatt tttaaaggac ggtgagttcc atg acc agc ccc gtg	115
Met Thr Ser Pro Val	
1 5	

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg	163
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp	
10 15 20	

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc	211
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu	
25 30 35	

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt	259
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe	
40 45 50	

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac	307
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His	
55 60 65	

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc	355
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Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly	
70					75					80					85	
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr	
			90						95					100		
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly	
			105					110					115			
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala	
			120				125					130				
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr	
			135				140				145					
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val	
150					155					160					165	
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr	
				170					175					180		
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys	
			185					190					195			
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln	
		200					205					210				
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met	
	215					220					225					
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg	
230					235				240						245	
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly	
				250					255					260		
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr	
			265					270					275			
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val	
		280					285					290				
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac	
1027																
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn	
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cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac
 1075
 Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp
 310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac
 1123
 Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr
 330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc
 1171
 Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr
 345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc
 1219
 Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile
 360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg
 1267
 Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met
 375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc
 1315
 Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu
 390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca
 1363
 Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala
 410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc
 1411
 Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly
 425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga
 1459
 Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly
 440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc
 1507
 Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr
 455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga
 1555
 Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg
 470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc
 1603
 Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys
 490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca
 1651
 Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser
 505 510 515

 agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc
 1699
 Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly
 520 525 530

 gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg
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 Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr
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 Ala Pro Phe Ser
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 <213> *Corynebacterium glutamicum*

<400> 266
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 Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
 35 40 45

 Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
 50 55 60

 His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
 65 70 75 80

 Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
 85 90 95

 Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
 100 105 110

 Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
 115 120 125

 Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
 130 135 140

 Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
 145 150 155 160

 Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
 165 170 175

 Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

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Glu	Ala	Gly	Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe				
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Glu	Ala	Val	Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr				
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Phe	Asp	Lys	Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile				
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Thr	Trp	Gly	Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val				
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Pro	Ser	Pro	Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu				
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Lys	Ala	Leu	Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp				
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Ile	Lys	Ile	Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile				
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Glu	Asp	Leu	Gln	Ile	Ala	Ala	Asp	Ile	Leu	Lys	Gly	His	Lys	Ile	Ala				
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Asp	Gly	Met	Arg	Met	Met	Val	Val	Pro	Ser	Ser	Thr	Trp	Ile	Lys	Gln				
385					390					395					400				
Glu	Ala	Glu	Ala	Leu	Gly	Leu	Asp	Lys	Ile	Phe	Thr	Asp	Ala	Gly	Ala				
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Glu	Trp	Arg	Thr	Ala	Gly	Cys	Ser	Met	Cys	Leu	Gly	Met	Asn	Pro	Asp				
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Gln	Leu	Lys	Pro	Gly	Glu	Arg	Ser	Ala	Phe	Thr	Ser	Asn	Arg	Asn	Phe				
	435						440					445							
Glu	Gly	Arg	Gln	Gly	Pro	Gly	Gly	Arg	Thr	His	Leu	Val	Ser	Pro	Ala				
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Val	Ala	Ala	Ala	Thr	Glu	Ser	Ala	Asp	Pro	Val	Leu	Thr	Cys	Arg	Tyr				
465					470					475					480				
Leu	Arg	Lys	Ala	Arg	Lys	Gln	Trp	Lys	Asn	Leu	Pro	Pro	Thr	Pro	Ala				
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Leu	Ala	Phe	His	Cys	Ser	Asp	Pro	Thr	Trp	Thr	Pro	Thr	Arg	Ser	Ser				
			500					505					510						

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
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Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
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Thr Pro Thr Arg Thr Ala Pro Phe Ser
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<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1602)

<223> FRXA01026

<400> 267

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ctc	ctc	tac	atc	gac	ctg	cag	ctg	ctg	cat	gaa	gtg	acc	tca	cca	cag	96
Leu	Leu	Tyr	Ile	Asp	Leu	Gln	Leu	Leu	His	Glu	Val	Thr	Ser	Pro	Gln	
			20					25					30			
gca	ttt	gac	ggc	ctg	cgc	atg	acc	ggc	cgt	aaa	ctg	cgc	cac	cca	gaa	144
Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	Leu	Arg	His	Pro	Glu	
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ctg	cac	ctg	gcc	acc	gaa	gac	cac	aac	gtg	cca	acc	gaa	ggc	atc	aag	192
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	
	50					55					60					
act	ggc	tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	240
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	
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tct	act	ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	288
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	
			85						90					95		
atg	ggt	gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	336
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	
			100					105					110			
ggc	gca	acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggt	gac	tcc	cac	acc	384
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	
		115					120					125				
tcc	acc	cac	ggt	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggt	acc	tca	432
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	
	130					135					140					
gag	gtt	gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	480
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	
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Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser	
165 170 175	
tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc	576
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly	
180 185 190	
gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg	624
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met	
195 200 205	
tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc	672
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly	
210 215 220	
gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt	720
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val	
225 230 235 240	
gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt	768
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val	
245 250 255	
gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag	816
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys	
260 265 270	
gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc	864
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly	
275 280 285	
acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca	912
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro	
290 295 300	
gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg	960
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Glu Lys Ala Leu	
305 310 315 320	
cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc	1008
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile	
325 330 335	
gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg	1056
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu	
340 345 350	
cag atc gcc gct gac atc ctg aag ggc cac aaa atc gcc gac ggc atg	1104
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met	
355 360 365	
cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa	1152
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu	
370 375 380	

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt
 1200
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag
 1248
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc
 1296
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc
 1344
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag
 1392
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc
 1440
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct
 1488
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca
 1536
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca
 1584
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc
 1625
 Arg Thr Ala Pro Phe Ser
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<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

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Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys															
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Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro															
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Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu															
			100					105					110																	
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr															
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Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser															
	130					135					140																			
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe															
145					150					155					160															
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser															
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Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly															
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Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly															
	210					215					220																			
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Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val															
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Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys															
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Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro															
	290					295					300																			
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305					310					315					320															
Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp	Ile	Lys	Ile															
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Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile	Glu	Asp	Leu															
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Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
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 515 520 525
 Arg Thr Ala Pro Phe Ser
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<210> 269

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN01127

<400> 269

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 Met Lys Leu Ala Val
 1 5
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 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
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 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

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ggc	gca	cgc	cgt	tac	ctc	aaa	aat	ggc	gag	ctg	ctc	acc	gac	gag	gat	259
Gly	Ala	Arg	Arg	Tyr	Leu	Lys	Asn	Gly	Glu	Leu	Leu	Thr	Asp	Glu	Asp	
40				45				50								
ctg	gca	tcc	ctg	cgc	gag	cat	gac	gcg	atc	ctt	ctt	ggc	gct	atc	ggc	307
Leu	Ala	Ser	Leu	Arg	Glu	His	Asp	Ala	Ile	Leu	Leu	Gly	Ala	Ile	Gly	
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gca	cca	ggc	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggc	ttg	ctg	ctg	355
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu	
70				75				80				85				
aag	atg	cga	ttc	gca	ctg	gat	cac	cac	gtg	aac	ctg	cgc	cca	tcc	aag	403
Lys	Met	Arg	Phe	Ala	Leu	Asp	His	His	Val	Asn	Leu	Arg	Pro	Ser	Lys	
90				95				100								
ctg	tac	gac	ggc	gtg	gag	tcc	cca	ctg	cgt	aac	cca	ggc	aag	att	gat	451
Leu	Tyr	Asp	Gly	Val	Glu	Ser	Pro	Leu	Arg	Asn	Pro	Gly	Lys	Ile	Asp	
105				110				115								
ttc	gtt	gtg	gtc	cgc	gaa	ggc	acc	gaa	ggc	gcc	tac	act	ggc	aac	ggc	499
Phe	Val	Val	Val	Arg	Glu	Gly	Thr	Glu	Gly	Ala	Tyr	Thr	Gly	Asn	Gly	
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gga	gca	atc	cgc	gtg	gga	acc	cct	cac	gag	att	gcc	aac	gaa	acc	tcc	547
Gly	Ala	Ile	Arg	Val	Gly	Thr	Pro	His	Glu	Ile	Ala	Asn	Glu	Thr	Ser	
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gtg	aac	act	cgc	tac	ggc	gct	gag	cgc	gtt	att	cgc	tac	gca	ttc	gag	595
Val	Asn	Thr	Arg	Tyr	Gly	Ala	Glu	Arg	Val	Ile	Arg	Tyr	Ala	Phe	Glu	
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ctg	gca	cag	agc	cgc	cgc	aag	aag	ctc	acc	ctc	gtg	cac	aag	acc	aac	643
Leu	Ala	Gln	Ser	Arg	Arg	Lys	Lys	Leu	Thr	Leu	Val	His	Lys	Thr	Asn	
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gtc	ctg	gtt	cac	ggc	ggc	ggc	ctg	tgg	cag	cgc	acc	gta	gat	gag	gtt	691
Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg	Thr	Val	Asp	Glu	Val	
185				190				195								
gca	aag	gaa	tac	cca	gag	gta	gcc	gtc	gat	tac	aac	cac	atc	gat	gca	739
Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr	Asn	His	Ile	Asp	Ala	
200				205				210								
gca	acc	atc	tat	ctg	gtc	act	gat	cct	tcc	cgc	ttc	gat	gtg	att	gtt	787
Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg	Phe	Asp	Val	Ile	Val	
215				220				225								
acc	gat	aac	ctc	ttc	ggc	gac	atc	ctc	acc	gat	gag	gca	ggc	gca	gtc	835
Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp	Glu	Ala	Gly	Ala	Val	
230				235				240				245				
tct	ggc	gga	att	ggc	ctc	gca	gca	tcc	ggc	aac	atc	gat	gcc	acg	ggc	883
Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn	Ile	Asp	Ala	Thr	Gly	
250				255				260								
acc	aac	cct	tcc	atg	ttc	gag	cca	gtc	cac	ggc	tct	gca	cca	gat	atc	931
Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly	Ser	Ala	Pro	Asp	Ile	
265				270				275								

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala
 280 285 290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa
 1027
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu
 295 300 305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att
 1075
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile
 310 315 320 325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc
 1120
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
 330 335 340

taaatttcaa cgccgacccc ctt
 1143

<210> 270
 <211> 340
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
 1 5 10 15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
 20 25 30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn
 100 105 110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
 115 120 125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile
 130 135 140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile
 145 150 155 160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu

165 170 175
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg
 180 185 190
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr
 195 200 205
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg
 210 215 220
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp
 225 230 235 240
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
 245 250 255
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
 260 265 270
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
 275 280 285
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
 290 295 300
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp
 305 310 315 320
 Asn Ser Gln Pro Ile Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys
 325 330 335
 Ala Leu Gln Ser
 340

<210> 271
 <211> 403
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> FRXA01132

<400> 271
 gccctgcatg atggggtagt ggggggttggt gggcaggtac gagctgtgat caatcagcta 60
 cactagtga gtcacatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
 25 30 35


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ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
      40                      45                      50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307
Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly
      55                      60                      65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
      70                      75                      80                      85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys
      90                      95                      100

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<210> 272
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 272
Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
  1                      5                      10                      15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
      20                      25                      30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
      35                      40                      45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
      50                      55                      60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
      65                      70                      75                      80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
      85                      90                      95

Leu Arg Pro Ser Lys
      100

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<210> 273
 <211> 1494
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1471)
 <223> RXN00536

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<400> 273
cgggcggtcc cagaggtctt aacacgaccg gcatcccgtc gcggagtttg gtgttgccgg 60

tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115
Met Ser Pro Asn Asp
      1                      5

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gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg
 1363
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg
 1411
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg
 1459
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser
 440 445 450

ctc cat gca ggt tgagttctcc accgttgtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
245 250 255

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg
 260 265 270
 Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly
 275 280 285
 Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu
 290 295 300
 Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
 305 310 315 320
 Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp
 325 330 335
 Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
 340 345 350
 Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
 355 360 365
 Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
 370 375 380
 Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
 385 390 395 400
 Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg
 405 410 415
 Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu
 420 425 430
 Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg
 435 440 445
 Ser Ala Asp Pro Ser Leu His Ala Gly
 450 455

<210> 275

<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> FRXA00536

<400> 275

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 tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115
 Met Ser Pro Asn Asp
 1 5
 gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
ggt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
ggt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275
 tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290
 ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305
 aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325
 atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340
 cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355
 cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370
 cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385
 cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405
 acc gaa tgg gag gtt cct
 1333
 Thr Glu Trp Glu Val Pro
 410

<210> 276

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
 1 5 10 15
 Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
 20 25 30
 Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

35					40					45					
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr
50						55					60				
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala
65					70					75					80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu
				85					90					95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala
			100					105					110		
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met
			115				120						125		
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His
						135					140				
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile
145					150					155					160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe
				165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu
			180					185					190		
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp
			195				200						205		
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys
						215						220			
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn
225					230					235					240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn
				245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg
			260					265					270		
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly
			275				280					285			
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu
						295					300				
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val
305					310					315					320
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp
				325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln
			340					345					350		
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr
			355				360					365			

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
 385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
 405 410

<210> 277

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

caggaggccg caccacacctg gatatcccccag cagtcgcagc cgccaccgaa tccgcggacc 60

ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115
 Met Glu Lys Phe Thr
 1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
 Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
 10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
 Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
 25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
 Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
 40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
 Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
 55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
 Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
 70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
 Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
 90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
 Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
 105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
 Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
 120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met
 150 155 160 165
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile
 170 175 180
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
 185 190 195
 taagtttcag tctgatagcg aaa 714

<210> 278

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg
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 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
 20 25 30
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln
 35 40 45
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190
 Pro Arg Thr Asn Ala



195

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<210> 279
<211> 936
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(913)  
<223> RXN01929
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Met Pro Met Ser Gly 5																
1																
att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163																
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val 20																
10 15																
aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211																
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala 35																
25 30																
cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259																
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser 40 45 50																
gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307																
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu 55 60 65																
gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355																
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg 70 75 80 85																
gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403																
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro 90 95 100																
aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451																
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala 105 110 115																
gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499																
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg 120 125 130																
cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547																
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr 135 140 145																
ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595																
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly 150 155 160 165																
gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643																

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 280

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130	135	140
His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val		
145	150	155 160
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg		
	165	170 175
Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro		
	180	185 190
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile		
	195	200 205
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln		
	210	215 220
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu		
225	230	235 240
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile		
	245	250 255
Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe		
	260	265 270

<210> 281

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 281

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tatttattct gagctgggtca tcacatctat actcatgccc	atg tca ggc att gat	115
	Met Ser Gly Ile Asp	
	1 5	

gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
	10 15 20

cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
	25 30 35

ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	
	40 45 50

aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
	55 60 65

atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
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Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu
 70 75 80 85

gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag 403
 Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln
 90 95 100

gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg 451
 Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala
 105 110 115

gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att 499
 Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile
 120 125 130

gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag 547
 Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln
 135 140 145

tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt 595
 Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser
 150 155 160 165

tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg 643
 Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala
 170 175 180

ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt 691
 Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val
 185 190 195

acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc 739
 Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly
 200 205 210

aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc 787
 Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg
 215 220 225

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 283

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01420

<400> 283

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gcggaatgcg	ctgctcatcc	acacgtggaa	tcttgattgg	gtg	acg	ctg	ggt	gga	115							
				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15					20			
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
			25					30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
		40					45					50				
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
	55					60					65					
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
70					75					80					85	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
				90				95						100		
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110					115			
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
	120					125					130					
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
	135					140					145					
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
150					155					160					165	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
				170					175					180		
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggt	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185					190					195			
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
		200					205					210				
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
	215					220					225					



ttc tat gca gtg gtg tgt ttc atc gtg tgc gtc att ctc gcg tgg gtg 835
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct
 1027
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta
 1065
 Thr Gly Ile Lys Ser
 310

<210> 284

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
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Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
 20 25 30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met



145					150					155					160
Ser	Val	Ile	Met	Ser 165	Leu	Pro	Met	Ala	Phe 170	Val	Val	Ala	Thr	Leu 175	Ala
Val	Arg	Asp	Ile 180	Glu	Gly	Lys	Ser	Gly 185	Glu	Ile	Ala	Ser	Pro 190	Arg	Ala
Val	Leu	Leu 195	Gly	Asn	Ile	Ser	Phe 200	Ala	Phe	Tyr	Met 205	Val	Gln	Phe	Pro
Val	Met 210	Val	Phe	Val	Gln	Arg 215	Tyr	Phe	Ile	Ala	Gly 220	Lys	Glu	Tyr	Gly
Phe 225	Leu	Gly	Trp	Ala	Phe 230	Tyr	Ala	Val	Val	Cys 235	Phe	Ile	Val	Ser	Val 240
Ile	Leu	Ala	Trp	Val 245	Leu	Phe	Thr	Phe	Val 250	Asp	Asp	Pro	Leu	Met 255	Lys
Ala	Thr	Ala	Arg 260	Lys	Lys	Gly	Ser	Arg 265	Arg	Leu	Lys	Gln	Ser 270	Asn	Ile
Leu	Val	Arg 275	Asp	Leu	Lys	Val	Leu 280	Phe	Gly	Lys	Ser	Pro 285	Glu	Lys	Pro
Leu	Lys 290	Val	Glu	Thr	Arg	Ala 295	Glu	Asn	Leu	Thr	Glu 300	Asn	Ser	Glu	Ala
Pro 305	Ala	Lys	Val	Ala	Thr 310	Gly	Ile	Lys	Ser						

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<210> 285
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1114)
<223> RXS01145
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Met Ala Ile Glu Leu
1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
40 45 50

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tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	



gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027
Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075
Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124
Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 286
<211> 338
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 286
Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190



Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335

Thr Ala

<210> 287

<211> 556

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA01145

<400> 287

taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
135 140 145

tgc ctc atc 556
Cys Leu Ile
150

<210> 288

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140



Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 289
<211> 1350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1327)
<223> RXA02375

<400> 289
cttttcaggt ctacgtgtat acgatggtaa cgctatgaat gatacgcaga acacacctga 60
aagcgttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115
Met Ala Pro Val Thr
1 5
ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
10 15 20
ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
25 30 35
gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
40 45 50
aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
55 60 65
gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
70 75 80 85
gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
90 95 100
gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
105 110 115
aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
120 125 130
gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
135 140 145
acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa	643
Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu	
170 175 180	
aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga	691
Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg	
185 190 195	
ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg	739
Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu	
200 205 210	
ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc	787
Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr	
215 220 225	
gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc	835
Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val	
230 235 240 245	
att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag	883
Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys	
250 255 260	
gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg	931
Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu	
265 270 275	
acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc	979
Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly	
280 285 290	
act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg	
1027	
Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp	
295 300 305	
gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc	
1075	
Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly	
310 315 320 325	
gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc	
1123	
Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly	
330 335 340	
att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc	
1171	
Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile	
345 350 355	
ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat	
1219	
Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp	
360 365 370	
tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca	
1267	
Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro	
375 380 385	

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr
390 395 400 405

gcc agc cgc gcg taaagcgcg gcctgctggt ggc
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala
1 5 10 15

Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His
115 120 125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile
130 135 140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

225 230 235 240
 Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly
 245 250 255
 Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly
 260 265 270
 Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu
 275 280 285
 Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser
 290 295 300
 Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile
 305 310 315 320
 Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser
 325 330 335
 Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly
 340 345 350
 Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly
 355 360 365
 Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln
 370 375 380
 Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp
 385 390 395 400
 Tyr Leu Ser Asn Tyr Ala Ser Arg Ala
 405

 <210> 291
 <211> 1419
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1396)
 <223> RXN02382

 <400> 291
 gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgatc 60

 cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr
 1 5

 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20

 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggc cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979



Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala
 280 285 290
 ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa
 1027
 Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu
 295 300 305
 gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat
 1075
 Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp
 310 315 320 325
 tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg
 1123
 Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val
 330 335 340
 gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa
 1171
 Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
 345 350 355
 gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc
 1219
 Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
 360 365 370
 gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat
 1267
 Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
 375 380 385
 ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa
 1315
 Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
 390 395 400 405
 ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag
 1363
 Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
 410 415 420
 tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca
 1416
 Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
 425 430
 agc
 1419
 <210> 292
 <211> 432
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 292
 Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
 1 5 10 15



Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile
 245 250 255
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser



340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln 355 360 365		
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser 370 375 380		
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly 385 390 395 400		
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu 405 410 415		
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro 420 425 430		

<210> 293
 <211> 724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(709)
 <223> FRXA02378

<400> 293
 gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgatc 60
 cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr
 1 5
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35
 acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
 40 45 50
 gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
 55 60 65
 ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
 70 75 80 85
 gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
 105 110 115

aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
 120 125 130

atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
 135 140 145

gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
 150 155 160 165

gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
 170 175 180

cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
 185 190 195

gcg gat ccg tcc aag att tgatcaccgg acgcg 724
 Ala Asp Pro Ser Lys Ile
 200

<210> 294

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
 1 5 10 15

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30

Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45

Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60

Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80

Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95

Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110

Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125

Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val



130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
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 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
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 Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (1)..(600)

<223> FRXA02382

<400> 295

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 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30
 cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45
 gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60
 gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80
 gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95
 ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336
 Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110
 ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125
 acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140



gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
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 Gln Gly Thr Gly Gln Ile Arg Pro
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<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

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 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro



195

200

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<211> 933
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<213> Corynebacterium glutamicum
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<223> RXA02499
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ctgctgcaaa acaggggtgg ttagtggcag tgtgggaacc																	atg	aca	aca	att	gct	115	
																	Met	Thr	Thr	Ile	Ala	5	
																	1						
gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc											163												
Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile																							
																	10	15	20				
gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa											211												
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu																							
																	25	30	35				
gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg											259												
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr																							
																	40	45	50				
gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg											307												
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val																							
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aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg											355												
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu																							
																	70	75	80	85			
gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc											403												
Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile																							
																	90	95	100				
agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg											451												
Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val																							
																	105	110	115				
cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act											499												
Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr																							
																	120	125	130				
gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag											547												
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys																							
																	135	140	145				
gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac											595												
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp																							
																	150	155	160	165			
atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc											643												



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Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe
      170                      175                      180

ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691
Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro
      185                      190                      195

cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739
Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala
      200                      205                      210

acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787
Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly
      215                      220                      225

gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835
Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu
      230                      235                      240

gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883
Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala
      250                      255                      260

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Asp Arg Ser Glu Glu Leu Gly Lys Arg
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tta 933

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<213> Corynebacterium glutamicum

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Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly
      35                      40                      45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
      50                      55                      60 -

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
      65                      70                      75                      80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
      85                      90                      95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
      100                      105                      110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
      115                      120                      125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

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130	135	140
Leu Glu Gln Val Lys Asp	Leu Leu Ser Thr Val Gly Asp Val Leu Glu	
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Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser		
165	170	175
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val		
180	185	190
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser		
195	200	205
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser		
210	215	220
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala		
225	230	235
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala		
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Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg		
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<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1273)

<223> RXS02157

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				Met Ser Thr Leu Glu	
				1	5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag	163	
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu		
10	15	20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc	211	
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val		
25	30	35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc	259	
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala		
40	45	50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt	307	
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly		
55	60	65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag	355
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His	Val	Ser	Asn	Leu	Phe	Ala	Ser	Arg	Pro	Val	Val	Glu	Val	Ala	Glu		
70					75				80						85		
gag	ctc	atc	aag	cgt	ttt	tcg	ctt	gac	gac	gcc	acc	ctc	gcc	gcg	caa	403	
Glu	Leu	Ile	Lys	Arg	Phe	Ser	Leu	Asp	Asp	Ala	Thr	Leu	Ala	Ala	Gln		
			90					95					100				
acc	cgg	gtt	ttc	ttc	tgc	aac	tcg	ggc	gcc	gaa	gca	aac	gag	gct	gct	451	
Thr	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu	Ala	Asn	Glu	Ala	Ala		
			105					110					115				
ttc	aag	att	gca	cgc	ttg	act	ggt	cgt	tcc	cgg	att	ctg	gct	gca	gtt	499	
Phe	Lys	Ile	Ala	Arg	Leu	Thr	Gly	Arg	Ser	Arg	Ile	Leu	Ala	Ala	Val		
		120					125					130					
cat	ggt	ttc	cac	ggc	cgc	acc	atg	ggt	tcc	ctc	gcg	ctg	act	ggc	cag	547	
His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu	Ala	Leu	Thr	Gly	Gln		
	135					140					145						
cca	gac	aag	cgt	gaa	gcg	ttc	ctg	cca	atg	cca	agc	ggt	gtg	gag	ttc	595	
Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro	Ser	Gly	Val	Glu	Phe		
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tac	cct	tac	ggc	gac	acc	gat	tac	ttg	cgc	aaa	atg	gta	gaa	acc	aac	643	
Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn		
			170					175						180			
cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggt	gaa	acg	691	
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr		
			185					190					195				
ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739	
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu		
		200					205					210					
tgc	gat	gag	tac	ggc	atc	ttg	atg	atc	acc	gat	gaa	gtc	cag	act	ggc	787	
Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	Glu	Val	Gln	Thr	Gly		
	215					220					225						
gtt	ggc	cgt	acc	ggc	gat	ttc	ttt	gca	cat	cag	cac	gat	ggc	gtt	gtt	835	
Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	His	Asp	Gly	Val	Val		
230					235					240					245		
ccc	gat	gtg	gtg	acc	atg	gcc	aag	gga	ctt	ggc	ggc	ggt	ctt	ccc	atc	883	
Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	Gly	Gly	Leu	Pro	Ile		
				250					255					260			
ggt	gct	tgt	ttg	gcc	act	ggc	cgt	gca	gct	gaa	ttg	atg	acc	cca	ggc	931	
Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	Leu	Met	Thr	Pro	Gly		
			265					270					275				
aag	cac	ggc	acc	act	ttc	ggt	ggc	aac	cca	gtt	gct	tgt	gca	gct	gcc	979	
Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala		
		280					285					290					
aag	gca	gtg	ctg	tct	gtt	gtc	gat	gac	gct	ttc	tgc	gca	gaa	gtt	gcc		
1027																	
Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	Cys	Ala	Glu	Val	Ala		
	295					300						305					



cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
1075

Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
1123

Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
1171

Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
1219

Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
1267

Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

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1296

Ile Ala

390

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<211> 391

<212> PRT

<213> Corynebacterium glutamicum

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Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
85 90 95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
100 105 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
115 120 125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
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 <223> RXS02262

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Met Thr Ala Thr Tyr
1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
55 60 65

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Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
90 95 100

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Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu
170 175 180

cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly
185 190 195

atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa 739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu
200 205 210

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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile
 215 220 225
 gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835
 Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro
 230 235 240 245
 tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca 883
 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro
 250 255 260
 gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931
 Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu
 265 270 275
 gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc 979
 Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly
 280 285 290
 cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac
 1027
 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp
 295 300 305
 ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc
 1075
 Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly
 310 315 320 325
 gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc
 1123
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
 330 335 340
 atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca
 1171
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355
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 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
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 35 40 45
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
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 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335



Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
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<213> Corynebacterium glutamicum

<220>

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<223> RXS02970

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 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly

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Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly			
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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc			643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr			
	170	175	180
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc			691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser			
	185	190	195
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys			
	200	205	210
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg			787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala			
	215	220	225
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca			835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro			
	230	235	240
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile			
	250	255	260
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa			931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys			
	265	270	275
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc			979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile			
	280	285	290
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1027			
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile			
	295	300	305
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1075			
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser			
	310	315	320
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1123			
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys			
	330	335	340
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1171			
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala			
	345	350	355
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa			
1219			
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			

360 365 370
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 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
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 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
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 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435
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 35 40 - 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

115					120					125					
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala
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Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr
145					150					155					160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
				165					170					175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
		195					200					205			
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala
210						215					220				
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
			245						250					255	
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
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Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe
		275					280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
	290						295				300				
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
				325					330					335	
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
			340					345					350		
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
	355						360					365			
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
	370					375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
385					390					395					400
Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
				405					410					415	
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
			420					425					430		
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu
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<223> FRXA01009

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Leu Ala Leu Lys Gly
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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027	
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075	
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310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123	
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330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
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1219	
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360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267	
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375

380

385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315

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1330

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35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210 215 220



Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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 <223> RXN00023

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 Met Thr Ser Met Asn
 1 5
 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
 10 15 20
 cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211
 Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp
 25 30 35

gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
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acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
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Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
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Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931
Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
 1027
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
 1315
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
 455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
 1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
 470 475 480 485
 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
 1603
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
 490 495 500
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
 1651
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
 505 510 515
 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
 1699
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
 520 525 530
 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
 1747
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
 535 540 545
 att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
 1795
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
 550 555 560 565
 atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
 1843
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
 570 575 580
 ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
 1891
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
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 gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
 1939
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
 600 605 610
 gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
 1987
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
 615 620 625 -
 gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
 2035
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
 630 635 640 645
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
 2083
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
 650 655 660
 tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
 2131
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

665					670					675				
aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc														
2179														
Asn Arg Asp Val Gly Cys Ala					Leu Ile Ser His Glu					His Val Asp Arg				
680					685					690				
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg														
2227														
Val Ile Leu Thr Gly Ser					Ser Glu Thr Ala Ala					Met Phe Ser Ser Trp				
695					700					705				
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc														
2275														
Arg Pro Glu Leu Thr					Ile Asn Gly Glu Thr					Ser Gly Lys Asn Ala Ile				
710					715					720 725				
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg														
2323														
Val Val Thr Pro					Ser Ala Asp Arg Asp					Leu Ala Val Ala Asp Leu Val				
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aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc														
2371														
Lys Ser Ala Phe Gly His Ala Gly					Gln Lys Cys Ser					Ala Ala Ser Leu				
745					750					755				
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag														
2419														
Gly Ile Leu Val Gly Ser Val					Tyr Glu Ser Glu Arg					Phe Arg Lys Gln				
760					765					770				
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc														
2467														
Leu Val Asp Ala Ala Ser					Ser Leu Ile Val Asp					Trp Pro Thr Asn Pro				
775					780					785				
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac														
2515														
Ser Ala Thr Val Gly Pro Leu Thr					Glu Leu Pro Ser					Asp Lys Leu His				
790					795					800 805				
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc														
2563														
His Ala Leu Thr Thr Leu Glu Glu Gly					Glu Ser Trp Leu Leu Lys Pro									
810					815					820				
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa														
2611														
Arg Gln Leu Asp Asp Thr Gly Arg					Leu Trp Ser Pro Gly					Ile Lys Glu				
825					830					835				
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca														
2659														
Gly Val Lys Pro Gly Thr Phe Phe					His Leu Thr Glu Val Phe Gly Pro									
840					845					850				
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc														
2707														
Val Leu Gly Leu Met Lys Ala Thr					Asp Leu Asn Glu Ala Ile Glu Phe									
855					860					865				

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
 2755
 Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
 870 875 880 885

 gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
 2803
 Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
 890 895 900

 tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
 2851
 Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
 905 910 915

 gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
 2899
 Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
 920 925 930

 ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
 2947
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
 935 940 945

 cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
 2995
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
 950 955 960 965

 gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
 3043
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
 970 975 980

 gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
 3091
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
 985 990 995

 gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga
 3139
 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
 1000 1005 1010

 ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca
 3187
 Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
 1015 1020 1025

 gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt
 3235
 Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
 1030 1035 1040 1045

 tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa
 3283
 Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
 1050 1055 1060

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac
 3331
 Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
 1065 1070 1075
 gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac
 3379
 Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
 1080 1085 1090
 act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac
 3427
 Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
 1095 1100 1105
 gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa
 3475
 Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys
 1110 1115 1120 1125
 gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg
 3523
 Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
 1130 1135 1140
 gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcattgggt
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 Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
 1145 1150
 cgc
 3579

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
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 Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
 35 40 45
 Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
 50 55 60
 Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80
 Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110



Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435					440					445					
Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
450					455					460					
Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
				485					490					495	
Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
			500					505					510		
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
		515					520					525			
Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala
		530				535					540				
Arg	Glu	Arg	Ala	Glu	Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val
545					550					555					560
Arg	Arg	Gly	His	Leu	Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala
				565					570					575	
Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
			580					585					590		
Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu
		595					600					605			
Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
		610				615					620				
Ile	Ala	Ile	Pro	Ala	Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala
625					630					635					640
Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
				645					650					655	
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His
			660					665					670		
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
		675					680					685			
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
		690				695					700				
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser
705					710					715					720
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
				725					730					735	
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys
			740				745					750			
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu
		755				760						765			

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
 885 890 895
 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
 915 920 925
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
 Glu Val Val Leu Arg Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala
 1010 1015 1020
 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu
 1025 1030 1035 1040
 Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
 1045 1050 1055
 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
 1060 1065 1070
 Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
 1105 1110 1115 1120

Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe
 1125 1130 1135

Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
 1140 1145 1150

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 <223> FRXA00023

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 1 5 10 15

gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
 20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
 115 120 125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu



130 135 140 476
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 Leu Ala Glu Glu Leu Lys Arg
 145 150

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 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
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 20 25 30
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
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 130 135 140
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 <222> (101)..(3124)
 <223> FRXA02284

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 Met Thr Ser Met Asn
 1 5

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
10 15 20	
cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883



Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile	Val	Leu	Gln	Ala	Tyr		
				250					255					260			
ctt	ccc	gat	gcc	ctc	ggg	gca	atc	cag	gac	ttg	gcg	cag	ttc	ggc	cgc	931	
Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg		
			265					270					275				
gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979	
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys		
		280					285					290					
ggg	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg		
1027																	
Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	Gln	Ile	Thr	Gly	Trp		
	295					300					305						
cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag		
1075																	
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys		
310					315					320					325		
cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc		
1123																	
Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	Met	Glu	Gly	Leu	Arg		
				330					335					340			
ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg		
1171																	
Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	Ala	Phe	Ala	His	Leu		
			345					350					355				
ctc	tct	gtg	gag	cgt	ggg	gta	gcg	gac	cgt	gtg	gag	ttc	gaa	atg	ctg		
1219																	
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu		
		360					365					370					
cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggg		
1267																	
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly		
	375					380					385						
gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg		
1315																	
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val		
390					395					400					405		
gcc	att	tct	tac	ctc	gtg	cgc	cgc	ctc	gag	gaa	aac	gcc	gcg	agc	gaa		
1363																	
Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	Asn	Ala	Ala	Ser	Glu		
				410					415					420			
aac	ttc	atg	tcc	gcc	atc	ttc	gac	ctc	gac	gcc	gac	aac	ccg	tcc	ttc		
1411																	
Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe		
			425					430					435				
aag	cga	gag	gag	agc	cgc	ttc	cgc	gcc	tcc	ata	tct	gac	ctc	gcc	acg		
1459																	
Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr		
		440					445					450					



ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser.
 455 460 465

 aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
 1555
 Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
 470 475 480 485

 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
 1603
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
 490 495 500

 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
 1651
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
 505 510 515

 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
 1699
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
 520 525 530

 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
 1747
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
 535 540 545

 att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
 1795
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
 550 555 560 565

 atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
 1843
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
 570 575 580

 ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
 1891
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
 585 590 595

 gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
 1939
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
 600 605 610

 gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
 1987
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
 615 620 625

 gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
 2035
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
 630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
 2083
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
 650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
 2131
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala
 665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc
 2179
 Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg
 680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg
 2227
 Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp
 695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc
 2275
 Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile
 710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg
 2323
 Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val
 730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc
 2371
 Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu
 745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag
 2419
 Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln
 760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc
 2467
 Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro
 775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac
 2515
 Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His
 790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc
 2563
 His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro
 810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa
 2611
 Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu
 825 830 835



ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca
 2659
 Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro
 840 845 850

 gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc
 2707
 Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe
 855 860 865

 caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
 2755
 Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
 870 875 880 885

 gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
 2803
 Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
 890 895 900

 tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
 2851
 Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
 905 910 915

 gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
 2899
 Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
 920 925 930

 ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
 2947
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
 935 940 945

 cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
 2995
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
 950 955 960 965

 gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
 3043
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
 970 975 980

 gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
 3091
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
 985 990 995

 gta gaa gcc aac att ttc cgc tac cga cca gca
 3124
 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 1000 1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum



<400> 312

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 1 5 10 15
 Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
 20 25 30
 Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
 35 40 45
 Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
 50 55 60
 Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80
 Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110
 Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Pro Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320



Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile
 435 440 445
 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His
 450 455 460
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro
 465 470 475 480
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln
 485 490 495
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu
 500 505 510
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu
 515 520 525
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala
 530 535 540
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val
 545 550 555 560
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala
 565 570 575
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg
 580 585 590
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu
 595 600 605
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro
 610 615 620
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala
 625 630 635 640
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala



645										650					655				
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His				
			660					665					670						
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His				
		675					680					685							
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala				
		690				695					700								
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser				
					710						715				720				
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala				
				725					730					735					
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys				
			740					745					750						
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu				
			755				760					765							
Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp				
						775						780							
Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro				
					790						795				800				
Ser	Asp	Lys	Leu	His	His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser				
				805					810					815					
Trp	Leu	Leu	Lys	Pro	Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser				
			820					825					830						
Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr				
			835				840					845							
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn				
			850			855					860								
Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly				
					870				875					880					
Leu	Gln	Ser	Leu	Asp	Ala	Asp	Glu	Val	Arg	Thr	Trp	Leu	Asp	His	Val				
				885					890					895					
Asp	Val	Gly	Asn	Ala	Tyr	Val	Asn	Arg	Gly	Ile	Thr	Gly	Ala	Ile	Val				
			900					905					910						
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly				
			915				920					925							
Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala				
						935					940								
Asp	Ala	Pro	Ser	His	His	Ala	Pro	Arg	Glu	Thr	Asn	Pro	Leu	Ile	Ser				
					950						955				960				
Lys	Leu	Asp	Leu	Pro	Gly	Glu	Glu	Leu	Glu	Trp	Leu	Glu	Lys	Ala	Asn				
				965				970						975					



Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
980 985 990

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
995 1000 1005

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<210> 313
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(904)  
<223> RXC02498
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<400> 313																
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aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115																
Met Ser Glu Glu Lys 5																
ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163																
Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser 20																
acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211																
Thr Asp Ala Pro Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly 35																
gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259																
Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys 50																
ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307																
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu 65																
cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355																
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu 85																
gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403																
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg 100																
ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451																
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu 115																
aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499																
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala 130																
gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547																

Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
 135 140 145
 gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595
 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
 150 155 160 165
 act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
 170 175 180
 gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
 185 190 195
 gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739
 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
 200 205 210
 tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg 787
 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
 215 220 225
 acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat 835
 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
 230 235 240 245
 ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
 250 255 260
 ggg ccg ctg gca atc gtc atg taatttgctg ttttgggccc ccg 927
 Gly Pro Leu Ala Ile Val Met
 265

<210> 314

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 314

Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
 1 5 10 15
 Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Ser
 20 25 30
 Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
 35 40 45
 Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
 50 55 60
 Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
 65 70 75 80
 Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
 85 90 95
 Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
 70 75 80 85
 tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
 90 95 100
 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
 105 110 115
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
 120 125 130
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
 135 140 145
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
 150 155 160 165
 acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
 170 175 180
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
 185 190 195
 ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210
 act gca gtg act tgaactggat ggagaggata cct 774
 Thr Ala Val Thr
 215

<210> 316

<211> 217

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
 1 5 10 15
 Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
 20 25 30
 Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45



Phe 50	Gly	Asp	Ala	Arg	Trp	Cys 55	Ala	His	Gln	Ala	Leu 60	Gln	Ala	Leu	Gly
Arg 65	Asp	Ser	Gly	Asp	Pro 70	Ile	Leu	Arg	Gly	Glu 75	Arg	Gly	Met	Pro	Leu 80
Trp	Pro	Ser	Ser	Val 85	Ser	Gly	Ser	Leu	Thr 90	His	Thr	Asp	Gly	Phe 95	Arg
Ala	Ala	Val	Val 100	Ala	Pro	Arg	Leu	Leu 105	Val	Arg	Ser	Met	Gly 110	Leu	Asp
Ala	Glu	Pro 115	Ala	Glu	Pro	Leu	Pro 120	Lys	Asp	Val	Leu	Gly 125	Ser	Ile	Ala
Arg 130	Val	Gly	Glu	Ile	Pro	Gln 135	Leu	Lys	Arg	Leu	Glu 140	Glu	Gln	Gly	Val
His 145	Cys	Ala	Asp	Arg	Leu 150	Leu	Phe	Cys	Ala	Lys 155	Glu	Ala	Thr	Tyr	Lys 160
Ala	Trp	Phe	Pro 165	Leu	Thr	His	Arg	Trp	Leu 170	Gly	Phe	Glu	Gln	Ala 175	Glu
Ile	Asp	Leu	Arg 180	Asp	Asp	Gly	Thr	Phe 185	Val	Ser	Tyr	Leu 190	Leu	Val	Arg
Pro	Thr	Pro 195	Val	Pro	Phe	Ile	Ser 200	Gly	Lys	Trp	Val	Leu 205	Arg	Asp	Gly
Tyr 210	Val	Ile	Ala	Ala	Thr	Ala 215	Val	Thr							

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<210> 317
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1264)
<223> RXA02155
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<400> 317
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gcaaacacaaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
Met Ala Glu Lys Gly
1 5
att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
10 15 20
aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
25 30 35
gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

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40	45	50	
cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala 55 60 65			307
gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala 120 125 130			499
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp 150 155 160 165			595
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu 170 175 180			643
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg
 1027
 Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
 295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att
 1075
 Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
 310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct
 1123
 Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
 330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga
 1171
 Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
 345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act
 1219
 Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
 360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct
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 Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
 375 380 385

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 1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala
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Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val
 20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Val Phe Thr Arg Asn
 35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp
 50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys
 65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu
 85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr
 100 105 110



Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile
 115 120 125
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala
 130 135 140
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val
 145 150 155 160
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met
 165 170 175
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala
 180 185 190
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala
 195 200 205
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp
 210 215 220
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln
 225 230 235 240
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala
 245 250 255
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr
 260 265 270
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr
 275 280 285
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro
 290 295 300
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met
 305 310 315 320
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu
 325 330 335
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala
 340 345 350
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
 355 360 365
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
 370 375 380
 Ala Tyr Ser Ser
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<210> 319

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA02156

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aacagcactc caactaaciaa gcagggaaaaa gggcacaggc atg aat gac ttg atc 115
 Met Asn Asp Leu Ile
 1 5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
 Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
 10 15 20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
 Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
 25 30 35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
 Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
 40 45 50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
 Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
 55 60 65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
 Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
 70 75 80 85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
 Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
 90 95 100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
 Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
 105 110 115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
 Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
 120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
 Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
 135 140 145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
 Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
 150 155 160 165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
 Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
 170 175 180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
 Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
 185 190 195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739



Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga
 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305

aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg
 1074
 Lys Asp Asp Lys Asp Gly Glu Leu
 310 315

<210> 320
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 320
 Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
 20 25 30

Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala
 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
 100 105 110

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
 115 120 125
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
 130 135 140
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
 145 150 155 160
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
 165 170 175
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
 180 185 190
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
 195 200 205
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
 210 215 220
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
 225 230 235 240
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
 245 250 255
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
 260 265 270
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
 275 280 285
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu
 290 295 300
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
 305 310 315

<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

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cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg acā atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

<210> 322
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322

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		20						25					30		
Leu	Gly	His	Pro	Ala	Tyr	Ala	Ser	Gly	Glu	Leu	Glu	Ile	Gly	Ala	Leu
		35					40					45			
Thr	Ala	Ala	Ser	Thr	Ala	Gly	Ser	Thr	Leu	Gly	Glu	Leu	Met	Pro	His
	50					55					60				
Ile	Pro	Gln	Leu	Ala	Asp	Arg	Val	Ile	Gln	Asp	Thr	Thr	Ala	Glu	Thr
65					70					75					80
Leu	Ala	Gly	His	Asp	Val	Val	Phe	Leu	Gly	Leu	Pro	His	Gly	Phe	Ser
				85					90					95	
Ala	Glu	Ile	Ala	Leu	Gln	Leu	Gly	Pro	Asp	Val	Thr	Val	Ile	Asp	Cys
			100					105					110		
Ala	Ala	Asp	Phe	Arg	Leu	Gln	Asn	Ala	Ala	Asp	Trp	Glu	Lys	Phe	Tyr
		115					120					125			
Gly	Ser	Glu	His	Gln	Gly	Thr	Trp	Pro	Tyr	Gly	Ile	Pro	Glu	Met	Pro
	130					135					140				
Gly	His	Arg	Glu	Ala	Leu	Arg	Gly	Ala	Lys	Arg	Val	Ala	Val	Pro	Gly
145					150					155				160	
Cys	Phe	Pro	Thr	Gly	Ala	Thr	Leu	Ala	Leu	Leu	Pro	Ala	Val	Gln	Ala
				165					170					175	
Gly	Leu	Ile	Glu	Pro	Asp	Val	Ser	Val	Val	Ser	Ile	Thr	Gly	Val	Ser
		180					185					190			
Gly	Ala	Gly	Lys	Lys	Ala	Ser	Val	Ala	Leu	Leu	Gly	Ser	Glu	Thr	Met
		195				200						205			
Gly	Ser	Leu	Lys	Ala	Tyr	Asn	Thr	Ser	Gly	Lys	His	Arg	His	Thr	Pro
	210					215					220				
Glu	Ile	Ala	Gln	Asn	Leu	Gly	Glu	Val	Ser	Asp	Lys	Pro	Val	Lys	Val
225					230					235				240	
Ser	Phe	Thr	Pro	Val	Leu	Ala	Pro	Leu	Pro	Arg	Glu	Phe	Ser	Pro	Leu
				245				250						255	
Gln	Pro	His	Leu												
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<210> 323



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<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(880)  
<223> FRXA02153
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Met Ile Met His Asn 5																
gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163																
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser 10 15 20																
gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211																
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala 25 30 35																
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259																
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr 40 45 50																
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307																
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala 55 60 65																
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355																
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp 70 75 80 85																
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403																
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu 90 95 100																
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451																
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg 105 110 115																
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499																
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln 120 125 130																
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547																
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala 135 140 145																
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595																
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly 150 155 160 165																
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643																
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro 170 175 180																
gat gtt tcc gta gtg tcc atc acc gcc gta tca ggt gca ggt aag aaa 691																



Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195
 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
 200 205 210
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
 215 220 225
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
 230 235 240 245
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
 250 255 260
 tgaaagaagg cgttaccgca gaa 903

 <210> 324
 <211> 260
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30
 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175



Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190
 Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205
 Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220
 Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240
 Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255
 Gln Pro His Leu
 260

<210> 325
 <211> 414
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA02154

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 caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5
 acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20
 acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35
 gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50
 gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
 55 60 65
 act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
 70 75 80 85
 gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
 90 95
 ccttaaagcg gcg 414



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<210> 326
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
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Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
      20             25             30
Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
      35             40             45
Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
      50             55             60
Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
      65             70             75             80
Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
      85             90             95
Pro

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<213> Corynebacterium glutamicum
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<222> (101)..(1273)
<223> RXA02157
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caccgttttt agaaaagacg acaaggatgg ggaactgtaa															115
										atg	agc	acg	ctg	gaa	
										Met	Ser	Thr	Leu	Glu	
										1				5	
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag															163
Thr	Trp	Pro	Gln	Val	Ile	Ile	Asn	Thr	Tyr	Gly	Thr	Pro	Pro	Val	Glu
				10					15					20	
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc															211
Leu	Val	Ser	Gly	Lys	Gly	Ala	Thr	Val	Thr	Asp	Asp	Gln	Gly	Asn	Val
			25					30					35		
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc															259
Tyr	Ile	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Val	Asn	Ala	Leu	Gly	His	Ala
		40					45					50			
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt															307
His	Pro	Ala	Ile	Ile	Glu	Ala	Val	Thr	Asn	Gln	Ile	Gly	Gln	Leu	Gly

55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag			355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu			
70	75	80	85
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa			403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln			
	90	95	100
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct			451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala			
	105	110	115
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt			499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val			
	120	125	130
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag			547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln			
	135	140	145
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc			595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe			
	150	155	160
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac			643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn			
	170	175	180
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg			691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr			
	185	190	195
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg			739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu			
	200	205	210
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc			787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly			
	215	220	225
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt			835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val			
	230	235	240
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc			883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile			
	250	255	260
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc			931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly			
	265	270	275
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc			979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala			
	280	285	290
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc			
1027			
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			



295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt
 1296
 Ile Ala
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 <213> Corynebacterium glutamicum
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 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115					120					125						
Ile	Leu	Ala	Ala	Val	His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu	
130					135					140						
Ala	Leu	Thr	Gly	Gln	Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro	
145					150					155					160	
Ser	Gly	Val	Glu	Phe	Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	
165					170					175						
Met	Val	Glu	Thr	Asn	Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	
180					185					190						
Ile	Gln	Gly	Glu	Thr	Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	
195					200					205						
Ala	Val	Arg	Glu	Leu	Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	
210					215					220						
Glu	Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	
225					230					235					240	
His	Asp	Gly	Val	Val	Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	
245					250					255						
Gly	Gly	Leu	Pro	Ile	Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	
260					265					270						
Leu	Met	Thr	Pro	Gly	Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	
275					280					285						
Ala	Cys	Ala	Ala	Ala	Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	
290					295					300						
Cys	Ala	Glu	Val	Ala	Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala	
305					310					315					320	
Lys	Val	Asp	Gly	Val	Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly	
325					330					335						
Val	Val	Leu	Glu	Arg	Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe	
340					345					350						
Lys	His	Gly	Val	Ile	Leu	Asn	Ala	Pro	Ala	Asp	Asn	Ile	Ile	Arg	Leu	
355					360					365						
Thr	Pro	Pro	Leu	Val	Ile	Thr	Asp	Glu	Glu	Ile	Ala	Asp	Ala	Val	Lys	
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Ala	Ile	Ala	Glu	Thr	Ile	Ala										
385					390											

<210> 329

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 329

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	
1315 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac	
1363 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His	
410 415 420	

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450

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 Ala Leu Phe
 455

<210> 330
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 <213> *Corynebacterium glutamicum*

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
 435 440 445
 Leu Thr Phe Ala Gly Ala Leu Phe
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<210> 331

<211> 1330

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 331

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ttattttaaaag acttcataat attttgggga gtgaactggg	ttg gca ttg aag ggt	115
	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163	
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
	10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211	
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
	25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259	
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
	40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307	
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
	55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355	
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
	70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403	
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
	90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451	
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
	105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499	
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
	120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547	
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
	135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595	
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
	150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643	
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
	170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691	
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
	185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739	
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys		
	200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787	
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
	215 220 225	

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atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230                235                240                245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
                250                255                260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
                265                270                275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
                280                285                290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
295                300                305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310                315                320                325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
                330                335                340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
                345                350                355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
                360                365                370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
                375                380                385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390                395                400                405

ttc aag gaa cgc ggc
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Phe Lys Glu Arg Gly
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<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum



<400> 332

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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320



Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
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Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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 <222> (101)..(1057)
 <223> RXA02158

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 Met Thr Ser Gln Pro
 1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
 10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
 25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
 40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
 55 60 65

ggt gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
 70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
 90 95 100



gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
 105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
 120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
 135 140 145

cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
 150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
 170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
 200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
 215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
 230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
 250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
 265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
 280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg
 1027
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
 295 300 305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc
 1077
 Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 310 315

aac
 1080

<210> 334
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 334

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			20					25					30		
Ala	Ala	Pro	Phe	Ser	Glu	Arg	Pro	Leu	Glu	Gly	Pro	Lys	Ser	Val	Ala
		35					40					45			
Val	Leu	Phe	Asp	Lys	Thr	Ser	Thr	Arg	Thr	Arg	Phe	Ser	Phe	Asp	Ala
	50					55					60				
Gly	Ile	Ala	His	Leu	Gly	Gly	His	Ala	Ile	Val	Val	Asp	Ser	Gly	Ser
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Ser	Gln	Met	Gly	Lys	Gly	Glu	Ser	Leu	Gln	Asp	Thr	Ala	Ala	Val	Leu
			85						90					95	
Ser	Arg	Tyr	Val	Glu	Ala	Ile	Val	Trp	Arg	Thr	Tyr	Ala	His	Ser	Asn
			100					105					110		
Phe	His	Ala	Met	Ala	Glu	Thr	Ser	Thr	Val	Pro	Leu	Val	Asn	Ser	Leu
		115					120					125			
Ser	Asp	Asp	Leu	His	Pro	Cys	Gln	Ile	Leu	Ala	Asp	Leu	Gln	Thr	Ile
	130					135					140				
Val	Glu	Asn	Leu	Ser	Pro	Glu	Glu	Gly	Pro	Ala	Gly	Leu	Lys	Gly	Lys
145					150					155					160
Lys	Ala	Val	Tyr	Leu	Gly	Asp	Gly	Asp	Asn	Asn	Met	Ala	Asn	Ser	Tyr
				165					170					175	
Met	Ile	Gly	Phe	Ala	Thr	Ala	Gly	Met	Asp	Ile	Ser	Ile	Ile	Ala	Pro
			180					185						190	
Glu	Gly	Phe	Gln	Pro	Arg	Ala	Glu	Phe	Val	Glu	Arg	Ala	Glu	Lys	Arg
		195				200						205			
Gly	Gln	Glu	Thr	Gly	Ala	Lys	Val	Val	Val	Thr	Asp	Ser	Leu	Asp	Glu
	210					215					220				
Val	Ala	Gly	Ala	Asp	Val	Val	Ile	Thr	Asp	Thr	Trp	Val	Ser	Met	Gly
225					230					235					240
Met	Glu	Asn	Asp	Gly	Ile	Asp	Arg	Thr	Thr	Pro	Phe	Val	Pro	Tyr	Gln
				245					250					255	
Val	Asn	Asp	Glu	Val	Met	Ala	Lys	Ala	Asn	Asp	Gly	Ala	Ile	Phe	Leu
			260				265						270		
His	Cys	Leu	Pro	Ala	Tyr	Arg	Gly	Lys	Glu	Val	Ala	Ala	Ser	Val	Ile
		275					280					285			

Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
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Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 305 310 315

<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXA02160

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 Met Thr Asn Arg Ile
 1 5

gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
 Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
 10 15 20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211
 Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
 25 30 35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
 Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
 40 45 50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
 Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
 55 60 65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
 Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
 70 75 80 85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
 Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
 90 95 100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
 Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
 105 110 115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
 Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
 120 125 130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
 Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
 135 140 145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595



Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro	
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Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile Asp Gln Asn Val Trp	
170 175 180	
ggc cgc gct att gag acc ggt tac ctg gaa gat ctg tgg aat gct cca	691
Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro	
185 190 195	
acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct	739
Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala	
200 205 210	
cca gat gag gtc atc atc tcc ttc gag ggt ggc aag cca gtc tcc atc	787
Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile	
215 220 225	
gat ggc cgt cca gtc tcc gta ctg cag gct att gaa gag ctg aac cgt	835
Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg	
230 235 240 245	
cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt	883
Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg	
250 255 260	
ctc gtg ggc atc aag tcc cgc gaa atc tac gaa gca cca ggc gca atc	931
Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile	
265 270 275	
gca ctg att aag gct cac gag gct ttg gaa gat gtc acc atc gag cgc	979
Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg	
280 285 290	
gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa	
1027	
Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala Arg Trp Ala Glu Glu	
295 300 305	
gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg	
1075	
Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala	
310 315 320 325	
ttc att gat tcc acc cag gag cac gtc acc ggc gat atc cgc atg gtt	
1123	
Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val	
330 335 340	
ctg cac gca ggt tcc atc acc atc aat ggt cgt cgt tcc agc cac tcc	
1171	
Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser	
345 350 355	
ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac	
1219	
Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp	
360 365 370	

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag
 1267
 Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
 375 380 385
 atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct
 1313
 Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
 390 395 400
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 1326

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 <211> 401
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 336
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 Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg
 35 40 45
 Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala
 50 55 60
 Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn
 65 70 75 80
 Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro
 85 90 95
 Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr
 100 105 110
 His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe
 115 120 125
 Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro
 130 135 140
 Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu
 145 150 155 160
 Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile
 165 170 175
 Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp
 180 185 190
 Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro
 195 200 205
 Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly
 210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile
 225 230 235 240
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp
 245 250 255
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu
 260 265 270
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp
 275 280 285
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala
 290 295 300
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys
 305 310 315 320
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly
 325 330 335
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg
 340 345 350
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365
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 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
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 Asn

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 <211> 1554
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1531)
 <223> RXN02162

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 Met Glu Gln His Gly
 1 5
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

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Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His														
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caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg														
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly														
	55					60					65																		
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg														
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu														
	70				75					80					85														
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac														
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp														
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cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc														
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg														
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aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg														
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val														
		120					125					130																	
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc														
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala														
	135					140					145																		
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc														
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe														
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cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca														
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala														
				170					175					180															
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt														
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg														
			185					190					195																
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg														
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu														
		200					205					210																	
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca														
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala														
	215					220					225																		
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa														
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu														
	230					235				240				245															
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cgc	ttg	gct														
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala														
			250						255					260															
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	ggg	tac	atc	acc	ttg														
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu														
		265						270					275																

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
 280 285 290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt
 1027
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac
 1075
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
 310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg
 1123
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
 330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg
 1171
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc
 1219
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc
 1267
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc
 1315
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt
 1363
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt
 1411
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt
 1459
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag
 1507
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 455 460 465

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 Trp Ala Arg Ala Gly Val Arg Arg
 470 475

<210> 338
 <211> 477
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45
 Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60
 Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80
 Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
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 Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
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 Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125
 Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140
 Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160
 Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
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 Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190
 Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205
 Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220
 Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
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<223> FRXA02161

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                                         Met Glu Gln His Gly
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acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser

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Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu														
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Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His														
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Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly														
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Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp														
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Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly														
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Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
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Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
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Tyr Val Pro Leu Gly
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Met Ser Arg Leu Ala																5
1																
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Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu																20
10 15																
tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac																211
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn																35
25 30																
cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt																259
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly																50
40 45																
aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac																307
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr																65
55 60																
aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg																355
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala																85
70 75 80 85																
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Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu																100
90 95																
acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc																451
Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr																115
105 110 115																
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Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe																130
120 125 130																
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Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser																145
135 140 145																
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Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val																165
150 155 160 165																
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Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly																180
170 175 180																

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 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
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<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met
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Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
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Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
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Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
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 <223> RXA02262

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 Met Thr Ala Thr Tyr
 1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
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aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
 70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
 90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
 105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
 Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
 120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
 Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
 135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
 Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
 150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
 Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu

170										175					180					
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Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly																				
185 190 195																				
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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile																				
215 220 225																				
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Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro																				
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Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro																				
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gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc	931																			
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu																				
265 270 275																				
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295 300 305																				
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1075																				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly																				
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1266																				
Asn Leu Trp Glu Ser Pro Ala Leu Ala																				
375 380																				

513

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Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe																									
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Ser	Asn	Thr	Gln	Pro																																				
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 <213> *Corynebacterium glutamicum*

<400> 346

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Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp
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Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly
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Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg
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Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp
	130					135						140			
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile
145					150					155					160
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr
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Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu
			180					185					190		
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser
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Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala
	210					215					220				
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met
225				230						235					240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala
				245					250					255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp
			260					265					270		
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp
		275					280					285			
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala



290

295

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Glu Thr Pro Glu His Ser Asn Thr Gln Pro
305 310

<210> 347

<211> 1662

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1639)

<223> RXA01508

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ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
Met Ser Asp Leu Gly
1 5

ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
10 15 20

tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
25 30 35

aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
40 45 50

gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
55 60 65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
70 75 80 85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
90 95 100

tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
105 110 115

ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
120 125 130

gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
135 140 145

gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
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atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
 375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
 390 395 400 405

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 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420

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 1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435

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 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
 440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
 455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat
 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac
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Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
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<210> 348

<211> 513

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<213> Corynebacterium glutamicum

<400> 348

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 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
 290 295 300
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
 340 345 350
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr
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Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val
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Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp
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His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly
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Asp

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 Met Pro Thr Ala Ser
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cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile
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gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp
 40 45 50

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Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu		
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Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	85	
70					75					80							
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Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	100	
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ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451	
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	115	
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gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499	
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	130	
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Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	145	
	135					140											
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595	
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	165	
	150					155				160							
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Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	180	
				170					175								
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691	
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	195	
			185					190									
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739	
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	210	
		200					205										
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787	
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	225	
	215					220											
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835	
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	245	
	230				235				240								
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883	
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	260	
				250					255								
gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	ttc	cc	ctg	ata		924	
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<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
          35           40           45
Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
          50           55           60
Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
 65           70           75           80
Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
          85           90           95
Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
          100          105          110
Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
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Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
          130          135          140
Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
          145          150          155          160
Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
          165          170          175
Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
          180          185          190
Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
          195          200          205
Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
          210          215          220
Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
          225          230          235          240
Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
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<222> (101)..(613)

<223> RXA02159

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 Met Ser Leu Gly Ser
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acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
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<213> Corynebacterium glutamicum

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Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly	35	40	45
Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly	50	55	60
Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly	65	70	75
Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys	85	90	95
Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly	100	105	110
Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala	115	120	125
Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala	130	135	140
Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys	145	150	155
Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr	165	170	

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<212> DNA

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Leu Lys Glu Gly Val	
1 5	

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa	163
Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu	
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acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca	211
Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala	
25 30 35	

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa	259
Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu	
40 45 50	



gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
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act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
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ccttaaagcg gcg 414

<210> 354

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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35 40 45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
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Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
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Pro

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<222> (101) .. (1279)

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Val Ser Lys Asp Thr
1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca
 1302
 Lys Lys Gly Ala
 390

<210> 356

<211> 393

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
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Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45



Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(901)

<223> RXS00905

<400> 357

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tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595



Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
 150 155 160 165
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
 170 175 180
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr
 185 190 195
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr
 200 205 210
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala
 215 220 225
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg
 230 235 240 245
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys
 250 255 260
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924
 Leu Glu Gly Arg Ala Leu
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<210> 358

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
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 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
 20 25 30
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
 35 40 45
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50 55 60
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65 70 75 80
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
 85 90 95
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
 100 105 110
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
 130 135 140
 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
 145 150 155 160
 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
 165 170 175
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
 180 185 190
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
 195 200 205
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
 210 215 220
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
 225 230 235 240
 Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
 245 250 255
 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
 260 265

<210> 359
 <211> 627
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> RXS00906

<400> 359
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 gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115
 Met Asn Thr Asp Ala
 1 5
 ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
 10 15 20
 tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
 25 30 35
 gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
 40 45 50
 cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
 55 60 65

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ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355
Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val
70 75 80 85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His
90 95 100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
105 110 115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
120 125 130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
135 140 145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
150 155 160 165

gtc aac cca taagcagaat tggcactcta cgg 627
Val Asn Pro

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<210> 360

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

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Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
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Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

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130 135 140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
 145 150 155 160

Thr Glu Leu Ile Glu Val Asn Pro
 165

<210> 361
 <211> 246
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> RXS00907

<400> 361
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actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
 Leu Ala Leu Tyr Gly
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35

aac tac acc aag tagaccctaaa agcaggcggtt aac 246
 Asn Tyr Thr Lys
 40

<210> 362
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 362
 Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
 1 5 10 15

Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
 20 25 30

Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35 40

<210> 363
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXS02001

<400> 363

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gcggtttcgt catggataag gactgtgttc gggaccattg cgataactcgt gtcaaaaggc 60

gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
                                         Met Pro Val Ile Asn
                                         1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
                        10                        15                        20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
                        25                        30                        35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
                        40                        45                        50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
                        55                        60                        65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
                        70                        75                        80                        85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
                        90                        95                        100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
                        105                        110                        115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
                        120                        125                        130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
                        135                        140                        145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
                        150                        155                        160                        165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
                        170                        175                        180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
                        185                        190                        195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
cgctcgaaga tgc 1281			
<210> 364			
<211> 386			
<212> PRT			
<213> Corynebacterium glutamicum			



<400> 364

Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
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Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
20 25 30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
35 40 45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
50 55 60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
65 70 75 80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
85 90 95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
100 105 110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
115 120 125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
130 135 140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
145 150 155 160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
165 170 175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
180 185 190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
195 200 205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
210 215 220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
225 230 235 240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala-Tyr Ile Asn Gly
245 250 255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
260 265 270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
275 280 285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
290 295 300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
305 310 315 320



<400> 365																
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Met Ser Arg Ile Ser																
1 5																
gaa ctt cta aac aat cat ggt gtt gat ctg tgg caa gag gcc gca																163
Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala																
10 15 20																
tat cag gat ttc cac gaa cat cct gag ctg tcc ggc ttc gaa tca gag																211
Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu																
25 30 35																
acc gca gat cgc att cag aaa tac ctg gag cgt ttt gat tgt gag gtg																259
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val																
40 45 50																
att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg																307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly																
55 60 65																
tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat																355
Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp																
70 75 80 85																
ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt																403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg																
90 95 100																
atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc																451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly																
105 110 115																

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
 Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
 135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
 Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
 150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
 Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
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His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
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Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu				
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Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala				
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Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg				
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Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser				
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Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala				
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Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile				
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Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr				
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Ala	Gly	Met	Leu	Arg	Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys				
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Ala	Ser	Asp	Ile	Arg	Glu	Gly	Val	Glu	Gly	Lys	Ser	Ile	Val	Asp	Arg				
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Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser				
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Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
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<211> 3221

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<213> *Corynebacterium glutamicum*

<220>

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<222> (1)..(3198)

<223> FRXA02234

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Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala	
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Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu	
35 40 45	
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Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly	
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Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala	
65 70 75 80	
att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc	288
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr	
85 90 95	
atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa	336
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu	
100 105 110	
gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca	384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro	
115 120 125	
tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa	432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu	
130 135 140	

gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca	480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	
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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	
165 170 175	
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Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	
180 185 190	
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Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	
195 200 205	
gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat	672
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp	
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Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	
225 230 235 240	
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Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	
245 250 255	
gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca	816
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	
260 265 270	
acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac	864
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	
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Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	
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1008	
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	
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1152	

Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
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 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca
 1248
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag
 1296
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
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 1344
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
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 1392
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
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 465 470 475 480
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 1488
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
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 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
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 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
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 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
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 1680
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
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 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp

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Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met				
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gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt																			
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gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg																			
2160																			
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu				
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gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg																			
2208																			
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu				
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tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag																			
2256																			
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu				
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gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg																			
2304																			
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		755					760					765							

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 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780

ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca
 2400
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc
 2448
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
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cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag
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 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830

gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat
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 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845

gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac
 2592
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 850 855 860

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 2640
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
 2688
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895

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 2736
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
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gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
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acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

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3221

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<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

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35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr



557



Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
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 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
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 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
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 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
 595 600 605
 Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
 610 615 620
 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
 625 630 635 640
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 645 650 655
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
 660 665 670
 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val
 675 680 685
 Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu
 690 695 700
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
 705 710 715 720
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
 725 730 735



Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
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 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
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 945 950 955 960
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 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
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1060

1065

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 <223> RXS02565

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 Val Asn Asp Leu Thr
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 cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
 Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
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 ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
 Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
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 gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
 Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
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 cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
 Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
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 gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
 Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
 105 110 115
 ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
 Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
 120 125 130
 gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
 Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
 135 140 145
 tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
 Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
 150 155 160 165
 gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

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Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg		
			185					190					195				
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
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gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
	215					220					225						
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
230					235					240					245		
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
				250				255						260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
			265					270					275				
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280					285					290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct		
1027																	
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
	295					300					305						
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct		
1075																	
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
310					315					320					325		
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg		
1123																	
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
				330					335					340			
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att		
1171																	
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
			345					350					355				
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg		
1219																	
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
		360					365					370					
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa		
1267																	
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu		
	375					380					385						

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat
 1315
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
 390 395 400 405
 ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta
 1363
 Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu
 410 415 420
 ggc taaaaacatg aagcaggagt ctt
 1389
 Gly

<210> 372
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
 1 5 10 15
 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
 20 25 30
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
 35 40 45
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
 50 55 60
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
 65 70 75 80
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
 85 90 95
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
 100 105 110
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
 115 120 125
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
 130 135 140
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
 145 150 155 160
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
 165 170 175
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
 180 185 190
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

<210> 373
 <211> 525
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(502)
 <223> RXS02937

<400> 373
 gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60
 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
 10 15 20
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
 25 30 35
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
 40 45 50
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
 55 60 65
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
 70 75 80 85
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
 90 95 100
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
 105 110 115
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
 120 125 130
 aaa taattggcta atgaatcctt ttc 525
 Lys

<210> 374

<211> 134

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 374

Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
 1 5 10 15
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
 20 25 30
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

100	105	110
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala		
115	120	125
Ser Ala Trp Leu Val Lys		
130		
<210> 375		
<211> 966		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(943)		
<223> RXA02194		
<400> 375		
gaaatctccc agctcattta ttggaccacag gtcacatcatgg ttgctcgcgg cctgaagcca 60		
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115		
		Met Leu Lys Ile Ala 5
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163		
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala	10	15 20
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211		
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe	25	30 35
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259		
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile	40	45 50
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307		
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg	55	60 65
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355		
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu	70	75 80 85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403		
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu	90	95 100
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451		
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro	105	110 115
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499		
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val	120	125 130
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547		
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala	135	140 145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739
Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
265 270 275

atc gcc cgc atc tagttttaac taccctcgaa aat 966
Ile Ala Arg Ile
280

<210> 376

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu
35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
85 90 95



Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile
 100 105 110
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly
 115 120 125
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile
 130 135 140
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg
 145 150 155 160
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr
 165 170 175
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu
 180 185 190
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn
 195 200 205
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala
 210 215 220
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala
 225 230 235 240
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala
 245 250 255
 Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu
 260 265 270
 Ala Ser Glu Ile Arg Ile Ala Arg Ile
 275 280

<210> 377

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02195

<400> 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccc aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115
 Met Tyr Arg Val Lys
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

	25	30	35	
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc				259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala				
	40	45	50	
gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att				307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile				
	55	60	65	
tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat				355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp				
	70	75	80	85
atc tac aag aac ctg taggagtttt aaagcaatca tgt				393
Ile Tyr Lys Asn Leu				
	90			

<210> 378

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
1 5 10 15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
20 25 30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
35 40 45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
50 55 60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
65 70 75 80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
85 90

<210> 379

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXA01097

<400> 379

gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaagggagc cattaaagat gcaggatttg aggtgcggaa atg agt gac aat cca	115
Met Ser Asp Asn Pro	
1 5	

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20

 gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Glu Ala Asp Gly Thr Asn Glu
 25 30 35

 gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50

 gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp
 55 60 65

 atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355
 Ile Lys Gly Leu Thr Ser Gly Asn Val Glu Glu Val Thr Gly Leu Ala
 70 75 80 85

 ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Glu Thr Gly
 90 95 100

 ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu
 105 110 115

 ctg taaaagcaac aacgattaag gaa 477
 Leu

<210> 380

<211> 118

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
 1 5 10 15

 Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
 20 25 30

 Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
 35 40 45

 Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
 50 55 60

 Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
 65 70 75 80

 Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
 85 90 95

 Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
 100 105 110

 Asp Asn Asp Val Leu Leu

115

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<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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<400> 381																60
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aaactggatc aactacatct aacagatagg atcaatatc																115
Met Thr Phe Thr Ile																5
1																
ctt	cct	gca	gtc	gat	gta	gtt	aac	gga	caa	gca	gtt	cgc	cta	gat	cag	163
Leu	Pro	Ala	Val	Asp	Val	Val	Asn	Gly	Gln	Ala	Val	Arg	Leu	Asp	Gln	20
10																
ggc	gag	gcc	ggc	act	gaa	aag	tct	tat	ggc	acc	cct	ttg	gaa	tcc	gca	211
Gly	Glu	Ala	Gly	Thr	Glu	Lys	Ser	Tyr	Gly	Thr	Pro	Leu	Glu	Ser	Ala	35
25																
ctg	aag	tgg	cag	gag	cag	ggt	gca	aag	tgg	ttg	cac	ttt	gtg	gac	ctg	259
Leu	Lys	Trp	Gln	Glu	Gln	Gly	Ala	Lys	Trp	Leu	His	Phe	Val	Asp	Leu	50
40																
gac	gca	gcg	ttc	aac	cgt	ggt	tcc	aac	cat	gag	atg	atg	gcg	gaa	att	307
Asp	Ala	Ala	Phe	Asn	Arg	Gly	Ser	Asn	His	Glu	Met	Met	Ala	Glu	Ile	65
55																
gtc	ggc	aag	ctc	gat	gtt	gat	gtg	gag	ctc	act	ggc	ggt	atc	cgt	gat	355
Val	Gly	Lys	Leu	Asp	Val	Asp	Val	Glu	Leu	Thr	Gly	Gly	Ile	Arg	Asp	85
70																
gat	gag	tct	ctg	gag	cgc	gcg	ctg	gca	acc	ggt	gca	cgt	cgt	gta	aac	403
Asp	Glu	Ser	Leu	Glu	Arg	Ala	Leu	Ala	Thr	Gly	Ala	Arg	Arg	Val	Asn	95
90																
att	ggt	acc	gct	gct	ctg	gag	aag	cca	gag	tgg	att	gct	tct	gcg	att	451
Ile	Gly	Thr	Ala	Ala	Leu	Glu	Lys	Pro	Glu	Trp	Ile	Ala	Ser	Ala	Ile	115
105																
caa	cgc	tat	ggc	gag	aag	att	gct	gtc	gat	atc	gct	gtg	cgt	ttg	gaa	499
Gln	Arg	Tyr	Gly	Glu	Lys	Ile	Ala	Val	Asp	Ile	Ala	Val	Arg	Leu	Glu	130
120																
gat	ggt	gaa	tgg	cgc	acc	cgt	gga	aac	ggt	tgg	gtc	tcc	gat	ggt	ggc	547
Asp	Gly	Glu	Trp	Arg	Thr	Arg	Gly	Asn	Gly	Trp	Val	Ser	Asp	Gly	Gly	145
135																
gat	ctg	tgg	gaa	gtt	ctc	gag	cgt	ttg	gat	tcc	caa	ggt	tgt	gca	cgt	595
Asp	Leu	Trp	Glu	Val	Leu	Glu	Arg	Leu	Asp	Ser	Gln	Gly	Cys	Ala	Arg	165
150																
ttc	gtg	gtt	acc	gat	gtg	tcc	aag	gac	ggc	acc	ttg	agt	ggt	cca	aat	643
155																
160																

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn
 170 175 180
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val
 185 190 195
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys
 200 205 210
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr
 215 220 225
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245
 ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

165 170 175
 Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr
 180 185 190
 Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val
 195 200 205
 Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile
 210 215 220
 Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala
 225 230 235 240
 Ala Val Glu Lys Leu Gly
 245

<210> 383
 <211> 756
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)
 <223> RXA01101

<400> 383
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 cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
 Met Thr Lys Thr Val
 1 5
 gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
 Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala
 10 15 20
 cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
 Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val
 25 30 35
 tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
 Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp
 40 45 50
 gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
 Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly
 55 60 65
 cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
 Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met
 70 75 80 85
 cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
 Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly
 90 95 100
 tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
 Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175	180	
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190	195	
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

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Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser
20 25 30

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly
35 40 45

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly
50 55 60

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly
65 70 75 80

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly
85 90 95

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu
100 105 110

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro
115 120 125

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr
130 135 140



Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
 145 150 155 160
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
 165 170 175
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
 180 185 190
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
 195 200 205
 Asn Tyr Ile
 210

<210> 385
 <211> 723
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXN01657

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 ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
 Val Ile Val Gly Val
 1 5
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
 10 15 20
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
 25 30 35
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
 40 45 50
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
 55 60 65
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
 70 75 80 85
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
 90 95 100
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165

caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp
 170 175 180

tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu
 185 190 195

ctg gcg att tgatgttttc ggtagcgctc tgt 723
 Leu Ala Ile
 200

<210> 386
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 386
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 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile
 195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

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 Val Ile Val Gly Val
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165

caa ggc 601
 Gln Gly

<210> 388
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
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Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly
 165

<210> 389
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA01098

<400> 389

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                                         Met Gly Val Ala Ile
                                         1                               5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10                               15                               20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25                               30                               35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40                               45                               50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55                               60                               65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70                               75                               80                               85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90                               95                               100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105                               110                               115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120                               125                               130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135                               140                               145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150                               155                               160                               165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170                               175                               180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185                               190                               195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200                               205                               210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val
 215 220 225
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val
 230 235 240 245
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys
 250 255
 tccacaagag tat 897

 <210> 390
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 390
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 20 25 30
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
 35 40 45
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
 50 55 60
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
 65 70 75 80
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
 85 90 95
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
 100 105 110
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
 115 120 125
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
 130 135 140
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
 145 150 155 160
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile
 165 170 175
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
 180 185 190
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
 195 200 205
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
 210 215 220



Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
 225 230 235 240
 Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
 245 250 255

Arg Lys

<210> 391
 <211> 729
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(706)
 <223> RXN01104

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 gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
 Met Thr Val Ala Pro
 1 5
 aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
 10 15 20
 gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
 25 30 35
 cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
 40 45 50
 gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
 55 60 65
 acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
 70 75 80 85
 att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
 90 95 100
 atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
 105 110 115
 tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
 120 125 130
 ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
 135 140 145
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
 150 155 160 165
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
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<210> 392

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

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 20 25 30
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

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Met Thr Val Ala Pro
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165



gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
Thr Lys Gly Ala Leu
200

<210> 394

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

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20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
195 200

<210> 395



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<211> 987
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(964)
<223> RXN00446
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				Met	Gly	Ala	Val	Glu									
					1			5									
ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	ggt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
				10					15					20			
acg	gta	ggt	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	ggt	cag	gca	211	
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
			25					30					35				
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
		40					45					50					
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	ggt	gcc	att	307	
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
	55					60					65						
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355	
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
70					75					80					85		
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403	
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
				90					95					100			
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451	
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
			105					110					115				
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499	
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe		
		120					125					130					
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547	
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
		135				140					145						
gac	aac	gtg	att	ggt	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595	
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
150					155					160				165			
ggc	ttg	cgt	gtt	ggt	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643	
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
				170					175					180			
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691	

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145 150 155 160		
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165 170 175		
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180 185 190		
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195 200 205		
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210 215 220		
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225 230 235 240		
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245 250 255		
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260 265 270		
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly 275 280 285		

<210> 397

<211> 545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA00446

<400> 397

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ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile 20 25 30	96
cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr 35 40 45	144
ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile 50 55 60	192
atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65                               70                               75                               80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg      288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                               85                               90                               95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg      336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
                               100                               105                               110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag      384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
                               115                               120                               125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att      432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
                               130                               135                               140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa      480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
                               145                               150                               155                               160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg              522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
                               165                               170

tagtcctttgg cgttttgcgg tgc                                          545

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<210> 398

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
                               20                               25                               30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
                               35                               40                               45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
                               50                               55                               60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65                               70                               75                               80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                               85                               90                               95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
                               100                               105                               110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
                               115                               120                               125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

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130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 399
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA01105

<400> 399
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
 Met Thr Lys Ile Thr
 1 5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
 10 15 20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
 25 30 35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
 40 45 50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
 55 60 65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
 70 75 80 85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
 90 95 100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
 105 110 115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
 120 125 130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
 135 140 145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt	595
Met Asp Val Ala Leu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027	
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075	
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123	
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171	
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218	
Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	

tga
1221

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<210> 400
<211> 366
<212> PRT
<213> Corynebacterium glutamicum
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<400> 400

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
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Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
50 55 60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
225 230 235 240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
245 250 255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
260 265 270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 401

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXA01106

<400> 401

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aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115
 Met Leu Asn Val Thr
 1 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu
 10 15 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro
 25 30 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr
 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala
 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355
 Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu
 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027	
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075	
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123	
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc
 1171
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly
 345 350 355
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac
 1219
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His
 360 365 370
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg
 1267
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr
 375 380 385
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct
 1315
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala
 390 395 400 405
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat
 1363
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp
 410 415 420
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc
 1411
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro
 425 430 435
 acc acc gac gag gcc taagaaaaat gacccaaatt act
 1449
 Thr Thr Asp Glu Ala
 440

<210> 402

<211> 442

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 402

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 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu
 20 25 30
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu
 35 40 45
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val	His	Ala	Glu	Gln	Lys	Pro	Ser	Glu	His	Thr	Thr	Glu	Leu	Ser	Pro	100	105	110
Gly	Gly	Thr	Val	Thr	Glu	Arg	Phe	Met	Pro	Ile	Asp	Arg	Val	Gly	Leu	115	120	125
Tyr	Val	Pro	Gly	Gly	Asn	Ala	Val	Tyr	Pro	Ser	Ser	Val	Ile	Met	Asn	130	135	140
Thr	Val	Pro	Ala	Gln	Glu	Ala	Gly	Val	Asn	Ser	Leu	Val	Val	Ala	Ser	145	150	155
Pro	Pro	Gln	Ala	Glu	His	Gly	Gly	Trp	Pro	His	Pro	Thr	Ile	Leu	Ala	165	170	175
Ala	Cys	Ser	Ile	Leu	Gly	Val	Asp	Glu	Val	Trp	Ala	Val	Gly	Gly	Gly	180	185	190
Gln	Ala	Val	Ala	Leu	Leu	Ala	Tyr	Gly	Asp	Asp	Ala	Ala	Gly	Leu	Glu	195	200	205
Pro	Val	Asp	Met	Ile	Thr	Gly	Pro	Gly	Asn	Ile	Phe	Val	Thr	Ala	Ala	210	215	220
Lys	Arg	Leu	Val	Arg	Gly	Val	Val	Gly	Thr	Asp	Ser	Glu	Ala	Gly	Pro	225	230	235
Thr	Glu	Ile	Ala	Val	Leu	Ala	Asp	Ala	Ser	Ala	Asn	Ala	Val	Asn	Val	245	250	255
Ala	Tyr	Asp	Leu	Ile	Ser	Gln	Ala	Glu	His	Asp	Val	Met	Ala	Ala	Ser	260	265	270
Val	Leu	Ile	Thr	Asp	Ser	Glu	Gln	Leu	Ala	Lys	Asp	Val	Asn	Arg	Glu	275	280	285
Ile	Glu	Ala	Arg	Tyr	Ser	Ile	Thr	Arg	Asn	Ala	Glu	Arg	Val	Ala	Glu	290	295	300
Ala	Leu	Arg	Gly	Ala	Gln	Ser	Gly	Ile	Val	Leu	Val	Asp	Asp	Ile	Ser	305	310	315
Val	Gly	Ile	Gln	Val	Ala	Asp	Gln	Tyr	Ala	Ala	Glu	His	Leu	Glu	Ile	325	330	335
His	Thr	Glu	Asn	Ala	Arg	Ala	Val	Ala	Glu	Gln	Ile	Thr	Asn	Ala	Gly	340	345	350
Ala	Ile	Phe	Val	Gly	Asp	Phe	Ser	Pro	Val	Pro	Leu	Gly	Asp	Tyr	Ser	355	360	365
Ala	Gly	Ser	Asn	His	Val	Leu	Pro	Thr	Ser	Gly	Ser	Ala	Arg	Phe	Ser	370	375	380
Ala	Gly	Leu	Ser	Thr	His	Thr	Phe	Leu	Arg	Pro	Val	Asn	Leu	Ile	Glu	385	390	395
Tyr	Asp	Glu	Ala	Ala	Leu	Lys	Asp	Val	Ser	Gln	Val	Val	Ile	Asn	Phe	405	410	415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala
 435 440

<210> 403
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXC00930

<400> 403
 acggcgccacc acacatttgg tgggtgtattg agctatctct gggctgcgtg agaaaccatt 60
 ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115
 Met Ser Gly His Ser
 1 5
 aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20
 ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
 25 30 35
 aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
 40 45 50
 aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
 55 60 65
 cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70 75 80 85
 atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
 90 95 100
 tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
 105 110 115
 atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
 120 125 130
 atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
 135 140 145
 gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
 150 155 160 165
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
 170 175 180
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 404

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
 1 5 10 15
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
 20 25 30
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
 210 215 220
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
 225 230 235 240
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
 245 250

<210> 405

<211> 547

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(547)

<223> RXC01096

<400> 405

accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
 Met Lys Pro Arg Val
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

<210> 406

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu				
1	5	10	15	
Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe				
	20	25	30	
Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp				
	35	40	45	
Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala				
	50	55	60	
Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile				
	65	70	75	80
Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu				
	85	90	95	
Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly				
	100	105	110	
Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala				
	115	120	125	
Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met				
	130	135	140	
Ile Gly Cys Ala Leu				
145				

<210> 407

<211> 1020

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (997)

<223> RXC01656

<400> 407

tcggcaagca tggcttcacg gtcctcaaaa aagtggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
 Met Thr Glu Thr Gln
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
 90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
 Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
 105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
 Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
 120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
 Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
 135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
 Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
 150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
 Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
 170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
 Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
 185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
 Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
 200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787



Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
 215 220 225
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
 230 235 240 245
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr
 250 255 260
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
 265 270 275
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
 280 285 290
 ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc
 1020
 Leu Ala Glu Arg Gly Trp
 295

<210> 408

<211> 299

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
 1 5 10 15
 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
 20 25 30
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
 115 120 125
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
 130 135 140
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
 165 170 175
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
 180 185 190
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
 195 200 205
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
 210 215 220
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
 225 230 235 240
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
 245 250 255
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
 260 265 270
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
 275 280 285
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
 290 295

<210> 409
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1042)
 <223> RXC01158

<400> 409
 taggacgttc aaggaattgg ctgaatcaac aagcgccaag gtggttaagc gccctcggcg 60
 agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag 115
 Met Ser Ile Val Glu
 1 5
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
 10 15 20
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
 25 30 35
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
 40 45 50
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
 55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta
 1065
 Phe Gly Asp Val Leu
 310

<210> 410
 <211> 314
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 410
 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
 1 5 10 15
 Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30
 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260 265 270
 Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
 275 280 285
 Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys
 290 295 300
 Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
 305 310

 <210> 411
 <211> 1413
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1390)
 <223> RXA02458

 <400> 411
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 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115
 Met Val Phe Val Ser
 1 5
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly
 10 15 20
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn
 25 30 35
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile
 40 45 50
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg
 55 60 65
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val
 70 75 80 85
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly
 90 95 100
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro
 105 110 115
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser
 120 125 130

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc	
1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg	
1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
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1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
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1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

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 1219
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu
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 1267
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp
 375 380 385
 cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc
 1315
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly
 390 395 400 405
 gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt
 1363
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
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ccg
 1413

<210> 412
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 <213> *Corynebacterium glutamicum*

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 35 40 45
 Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
 50 55 60
 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
 65 70 75 80
 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
 85 90 95
 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
 100 105 110
 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
 115 120 125
 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
 130 135 140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro
 145 150 155 160
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
 165 170 175
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
 180 185 190
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
 195 200 205
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
 210 215 220
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
 275 280 285
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
 290 295 300
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
 305 310 315 320
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
 325 330 335
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala
 340 345 350
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu
 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp
 370 375 380
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly
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<210> 413

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1243)
 <223> RXA02790

<400> 413

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                                         Met Glu Pro Val Tyr
                                         1                               5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
                               10                               15                               20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
                               25                               30                               35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
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gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307
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Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
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aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln
                               90                               95                               100

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Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
                               105                               110                               115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
                               120                               125                               130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
                               135                               140                               145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
                               150                               155                               160                               165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
                               170                               175                               180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
                               185                               190                               195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

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Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser
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 aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac 787
 Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn
 215 220 225
 cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt 835
 His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu
 230 235 240 245
 act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca 883
 Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala
 250 255 260
 cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc 931
 Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu
 265 270 275
 gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg 979
 Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu
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 1027
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
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 cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
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 330 335 340
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 1171
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 345 350 355
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 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
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 Ser Gly Val Leu Asp Ser Asn Arg
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<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

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Ala Thr Ser Asn	Arg Thr Pro His	Asp Tyr Glu Gly	Ser Gly Asn Gly
35	40	45	
Val Val Gln Leu	Val Glu Ile Pro	Glu Gly Ser Ser	Ile Ser Glu Leu
50	55	60	
Gly Pro Glu Leu	Glu Glu Arg Asp	Ile Val Ala Thr	Asn Ser Ala Phe
65	70	75	80
Gln Thr Ala Ala	Ser Asn Asn Pro	Asn Ala Gly Ser	Val Gln Pro Gly
85	90	95	
Phe Tyr Arg Leu	Gln Glu Gln Met	Asn Ala Ala Ala	Ala Val Ser Ala
100	105	110	
Leu Leu Asp Pro	Asp Asn Gln Val	Asp Leu Leu Asp	Ile His Gly Gly
115	120	125	
Ala Thr Leu Met	Asp Val Thr Val	Val Gly Gly Asn	Thr Arg Ala Gly
130	135	140	
Ile Tyr Ser Gln	Ile Ala Ala Val	Thr Cys Thr Glu	Gly Ser Ala Asn
145	150	155	160
Cys Ile Thr Ala	Glu Asp Leu Gln	Gln Val Ala Ser	Thr Val Ser Pro
165	170	175	
Ala Glu Leu Gly	Val Pro Asp Trp	Ala Ile Ala Ala	Val Glu Ala Arg
180	185	190	
Gly Thr Asp Pro	Lys Arg Leu Glu	Gly Leu Ile Met	Pro Gly Gln Tyr
195	200	205	
Val Val Asp Pro	Ser Asn Asp Ala	Gln Gly Ile Leu	Thr Asp Leu Ile
210	215	220	
Thr Arg Ser Ala	Asn His Phe Gln	Glu Thr Asp Ile	Thr Gly Arg Ala
225	230	235	240
Asp Ala Ile Gly	Leu Thr Pro Tyr	Glu Leu Val Thr	Ala Ala Ser Leu
245	250	255	
Ile Glu Arg Glu	Ala Pro Ala Gly	Asp Phe Asp Lys	Val Ala Arg Val
260	265	270	
Ile Leu Asn Arg	Leu Ala Glu Pro	Met Gln Leu Gln	Phe Asp Ser Thr
275	280	285	
Val Asn Tyr Gly	Leu Ser Glu Gln	Glu Val Ala Thr	Thr Asp Glu Asp
290	295	300	
Arg Gln Thr Val	Thr Pro Trp Asn	Thr Tyr Ala Met	Asp Gly Leu Pro
305	310	315	320
Gln Thr Pro Ile	Ala Ala Val Ser	Thr Glu Ala Leu	Gln Ala Met Glu
325	330	335	

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
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Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
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<210> 415

<211> 644

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	Val	Arg	Gln	Ala	Leu	
			20					25					30			
aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	ttg	ctg	tcc	ccg	gcg	144
Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	Leu	Leu	Ser	Pro	Ala	
		35					40					45				
cgc	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	gcc	aat	cat	gga	cag	192
Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	Ala	Asn	His	Gly	Gln	
		50				55					60					
ctc	atc	gcc	gag	gtc	ttc	cgc	gag	ttg	ggc	cgt	aca	cgc	gcg	ctt	gtt	240
Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	Thr	Arg	Ala	Leu	Val	
65				70					75					80		
gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	cac	ggc	acc	acc	ttg	288
Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	His	Gly	Thr	Thr	Leu	
				85					90					95		
gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	cat	tac	acc	atc	gag	336
Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	His	Tyr	Thr	Ile	Glu	
			100					105					110			
cct	gag	gac	ctt	ggc	ctt	ggc	cgc	tac	acc	ctt	gag	gat	ctc	gta	ggt	384
Pro	Glu	Asp	Leu	Gly	Leu	Gly	Arg	Tyr	Thr	Leu	Glu	Asp	Leu	Val	Gly	
		115					120					125				
ggc	ctc	ggc	act	gag	aac	gcc	gaa	gct	atg	cgc	gct	act	ttc	gcg	ggc	432
Gly	Leu	Gly	Thr	Glu	Asn	Ala	Glu	Ala	Met	Arg	Ala	Thr	Phe	Ala	Gly	
	130					135					140					
acc	ggc	cct	gat	gca	cac	cgt	gat	gcg	ttg	gct	gcg	tcc	gca	ggt	gcg	480
Thr	Gly	Pro	Asp	Ala	His	Arg	Asp	Ala	Leu	Ala	Ala	Ser	Ala	Gly	Ala	
145					150					155					160	

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
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tagtaataat ctgcccacag tgt 644

<210> 416

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
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Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

<210> 417
 <211> 611
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(588)
 <223> FRXA00954

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 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
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 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
 35 40 45
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
 50 55 60
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
 65 70 75 80
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
 85 90 95
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
 100 105 110
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
 115 120 125
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
 130 135 140
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
 145 150 155 160
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
 165 170 175
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
 180 185 190
 tct tcc aat gac tagtaataat ctgccacag tgt 611

Ser Ser Asn Asp
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<210> 418
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
35 40 45
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
50 55 60
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
65 70 75 80
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
85 90 95
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
100 105 110
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
115 120 125
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
130 135 140
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
145 150 155 160
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
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Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
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Ser Ser Asn Asp
195

<210> 419
<211> 1677
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1654)
<223> RXN00957

<400> 419

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Met Ser Thr Asn Pro
1 5
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His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu
10 15 20
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
25 30 35
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
40 45 50
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
55 60 65
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
70 75 80 85
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
90 95 100
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451
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gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
120 125 130
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
135 140 145
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Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
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Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
170 175 180
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu
185 190 195
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu
200 205 210
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag
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 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc
 1075
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat
 1123
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag
 1171
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg
 1219
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat
 1267
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca
 1315
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg
 1363
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc
 1411
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile
505 510 515

cga tgacacacgt tgttctcatt gat
1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu
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Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp
20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser
 500 505 510

Thr Leu Glu Val Ile Arg
 515

<210> 421
 <211> 1151
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1128)
 <223> FRXA00957

<400> 421
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 Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
 1 5 10 15

aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac 96
 Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
 20 25 30

atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc 144
 Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
 35 40 45

cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac 192
 Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
 50 55 60

gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac 240
 Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
 65 70 75 80

ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc 288
 Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
 85 90 95

acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac 336
 Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
 100 105 110

caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc 384
 Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
 115 120 125

gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc 432
 Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc tat gaa ctt ttt ggc gca			480
Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala			
145	150	155	160
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag			528
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln			
	165	170	175
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc			576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly			
	180	185	190
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act			624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr			
	195	200	205
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc			672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg			
	210	215	220
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat			720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp			
	225	230	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt			768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg			
	245	250	255
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg			816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg			
	260	265	270
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct			864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala			
	275	280	285
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt			912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Gly Ser Tyr Gly			
	290	295	300
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att			960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile			
	305	310	315
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct			
1008			
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala			
	325	330	335
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag			
1056			
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu			
	340	345	350
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct			
1104			
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala			
	355	360	365

ggt tcc act ttg gag gtc atc cga tgacacacgt tgttctcatt gat
 1151
 Gly Ser Thr Leu Glu Val Ile Arg
 370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Asn	Thr	Tyr	Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp
			20					25					30		
Ile	Asn	His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala
	35						40					45			
Pro	Gly	Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp
	50					55					60				
Ala	Ala	Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp
	65				70					75					80
Gly	Asp	Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg
				85					90					95	
Thr	Gln	Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr
			100					105					110		
Gln	Val	Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe
	115						120					125			
Ala	Ala	Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe
	130					135					140				
Tyr	Ile	Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala
145				150						155					160
Ser	Pro	Glu	Ser	Asn	Leu	Lys	Phe	Thr	Ala	Ala	Asn	Arg	Glu	Leu	Gln
				165					170					175	
Leu	Tyr	Pro	Ile	Ala	Gly	Thr	Arg	Pro	Arg	Gly	Leu	Asn	Pro	Asp	Gly
			180					185					190		
Ser	Ile	Asn	Asp	Glu	Leu	Asp	Ile	Arg	Asn	Glu	Leu	Asp	Met	Arg	Thr
	195						200					205			
Asp	Ala	Lys	Glu	Ile	Ala	Glu	His	Thr	Met	Leu	Val	Asp	Leu	Ala	Arg
	210					215					220				
Asn	Asp	Leu	Ala	Arg	Val	Ser	Val	Pro	Ala	Ser	Arg	Arg	Val	Ala	Asp
225					230					235					240
Leu	Leu	Gln	Val	Asp	Arg	Tyr	Ser	Arg	Val	Met	His	Leu	Val	Ser	Arg
			245						250					255	
Val	Thr	Ala	Thr	Leu	Asp	Pro	Glu	Leu	Asp	Ala	Leu	Asp	Ala	Tyr	Arg



260							265					270				
Ala	Cys	Met	Asn	Met	Gly	Thr	Leu	Thr	Gly	Ala	Pro	Lys	Leu	Arg	Ala	
275							280					285				
Met	Glu	Leu	Leu	Arg	Gly	Val	Glu	Lys	Arg	Arg	Arg	Gly	Ser	Tyr	Gly	
290							295					300				
Gly	Ala	Val	Gly	Tyr	Leu	Arg	Gly	Asn	Gly	Asp	Met	Asp	Asn	Cys	Ile	
305							310					315				
Val	Ile	Arg	Ser	Ala	Phe	Val	Gln	Asp	Gly	Val	Ala	Ala	Val	Gln	Ala	
320							325					330				
Gly	Ala	Gly	Val	Val	Arg	Asp	Ser	Asn	Pro	Gln	Ser	Glu	Ala	Asp	Glu	
335							340					345				
Thr	Leu	His	Lys	Ala	Tyr	Ala	Val	Leu	Asn	Ala	Ile	Ala	Leu	Ala	Ala	
350							355					360				
Gly	Ser	Thr	Leu	Glu	Val	Ile	Arg									
365							370					375				

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<210> 423
<211> 1068
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1045)
<223> RXA02687
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<400> 423
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tggacaccca ccttagttcg gcgggttaag ctgtgtaacc atg agc gac gca cca 115
Met Ser Asp Ala Pro
1 5

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163
Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala
10 15 20

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211
Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu
25 30 35

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259
Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His
40 45 50

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307
Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly
55 60 65

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355
Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln
70 75 80 85

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atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
 Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc
 1027
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att
 1068
 Glu Gly Arg Lys Leu Asn
 310 315

<210> 424

<211> 315

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 424

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Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr
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Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
          20              25              30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
      35              40              45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
      50              55              60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
      65              70              75              80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
          85              90              95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
      100              105              110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
      115              120              125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
      130              135              140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser
      145              150              155              160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
          165              170              175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
      180              185              190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
      195              200              205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
      210              215              220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
      225              230              235              240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
          245              250              255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
          260              265              270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
      275              280              285

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Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp
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Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

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gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa	595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu	
150 155 160 165	
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc	643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser	
170 175 180	
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc	691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile	
185 190 195	
gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg	739
Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Ser Met	
200 205 210	
atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc	787
Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly	
215 220 225	
atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac	835
Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His	
230 235 240 245	
att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg	883
Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met	
250 255 260	
ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa	931
Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu	
265 270 275	
gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac	979
Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp	
280 285 290	
aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc	
1027	
Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly	
295 300 305	
atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att	
1075	
Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile	
310 315 320 325	
tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag	
1123	
Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys	
330 335 340	
gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc	
1171	
Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala	
345 350 355	
gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca	
1219	
Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala	
360 365 370	

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac
 1267
 Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn
 375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt
 1315
 Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly
 390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc
 1353
 Leu Glu Asp Gly Ala
 410

<210> 426
 <211> 410
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 426
 Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln
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 Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr
 20 25 30
 Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
 35 40 45
 Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
 50 55 60
 Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
 65 70 75 80
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 85 90 95
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 100 105 110
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 115 120 125
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 130 135 140
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 145 150 155 160
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 165 170 175
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 180 185 190
 Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 210 215 220
 Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 225 230 235 240
 Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 245 250 255
 Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 260 265 270
 Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 275 280 285
 Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 290 295 300
 Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 305 310 315 320
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 370 375 380
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 385 390 395 400
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 405 410

<210> 427

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> FRXA01698

<400> 427

ggc aac act gag tgg gat aag tgg acc acc atc atg tcc tct gac gct 48
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35	40	45	
atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser 50 55 60			192
tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg 65 70 75 80			240
tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile 85 90 95			288
tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala 100 105 110			336
gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp 115 120 125			384
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly 130 135 140			432
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile 145 150 155 160			480
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile 165 170 175			528
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly 180 185 190			576
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu 195 200 205			624
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220			672
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240			720
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255			768
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270			816
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285			864

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Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met
 70              75              80              85

ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat    403
Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp
              90              95              100

atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat    451
Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp
              105              110              115

ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc    499
Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile
              120              125              130

gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa    547
Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu
              135              140              145

tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct    595
Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser
              150              155              160              165

gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca    643
Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr
              170              175              180

gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct    691
Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro
              185              190              195

gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc    739
Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg
              200              205              210

att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca    787
Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala
              215              220              225

cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc    835
Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr
              230              235              240              245

aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt    883
Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg
              250              255              260

tgaagaggtg ctctgtggtc agc    906

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<210> 430

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

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Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile
  1              5              10              15

```

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Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser
 20              25              30

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Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu
 130 135 140
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met
 145 150 155 160
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val
 165 170 175
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly
 180 185 190
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro
 195 200 205
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu
 210 215 220
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His
 225 230 235 240
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro
 245 250 255
 Ala Cys Pro Ser Arg
 260

<210> 431

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1522)

<223> RXA00955

<400> 431

gatggtgcac aaaaggcgct ttccttgctt gccgacggca ccaccagggc atggttgaggc 60

aagcacgaag agatcgatta ctcaaaaag gagtcttcca atg act agt aat aat 115

	Met	Thr	Ser	Asn	Asn	
	1				5	
ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg						163
Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu						
	10				20	
gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca						211
Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro						
	25			30	35	
aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg						259
Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly						
	40			45	50	
gcg cgt ttc atc atg gag tgc aag tcc gca tcc cct tct ttg gga atg						307
Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met						
	55			60	65	
att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc						355
Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala Arg Val Tyr Ser Arg						
	70			75	80	85
tac gcc agc ggc att tcc gtg ctg tgc gag ccg gat cgt ttt ggt ggc						403
Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro Asp Arg Phe Gly Gly						
	90			95	100	
gat tac gat cac ctc gct acc gtt gcc gct acc tct cat ctt ccg gtg						451
Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr Ser His Leu Pro Val						
	105			110	115	
ctg tgc aaa gac ttc atc att gat cct gtc cag gta cac gcg gcg cgt						499
Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln Val His Ala Ala Arg						
	120			125	130	
tac ttt ggt gct gat gcc atc ctg ctc atg ctc tct gtg ctt gat gat						547
Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu Ser Val Leu Asp Asp						
	135			140	145	
gaa gag tac gca gca ctc gct gcc gag gct gcg cgt ttt gat ctg gat						595
Glu Glu Tyr Ala Ala Leu Ala Glu Ala Ala Arg Phe Asp Leu Asp						
	150			155	160	165
atc ctc acc gag gtt att gat gag gag gaa gtc gcc cgc gcc atc aag						643
Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val Ala Arg Ala Ile Lys						
	170			175	180	
ctg ggt gcg aag atc ttt ggc gtc aac cac cgc aac ctg cat gat ctg						691
Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg Asn Leu His Asp Leu						
	185			190	195	
tcc att gat ttg gat cgt tca cgt cgc ctg tcc aag ctc att cca gca						739
Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser Lys Leu Ile Pro Ala						
	200			205	210	
gat gcc gtg ctc gtg tct gag tct ggc gtg cgc gat acc gaa acc gtc						787
Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg Asp Thr Glu Thr Val						
	215			220	225	
cgc cag cta ggt ggg cac tcc aat gca ttc ctc gtt ggc tcc cag ctg						835
Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu Val Gly Ser Gln Leu						

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys	310	315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga

1545

Ser Thr Phe His Tyr

470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
 385 390 395 400
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
 405 410 415
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
 420 425 430
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
 435 440 445
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
 450 455 460
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
 465 470

<210> 433
 <211> 494
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1) .. (471)
 <223> RXA02814

<400> 433

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gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1                      5                      10                      15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
                20                      25                      30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
                35                      40                      45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
                50                      55                      60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65                      70                      75                      80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
                85                      90                      95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
                100                      105                      110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
                115                      120                      125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
                130                      135                      140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
145                      150                      155

tcttaaaaca ccg 494

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<210> 434

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1                      5                      10                      15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
                20                      25                      30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
                35                      40                      45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
  50                      55                      60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
 65 70 75 80
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
 85 90 95
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
 100 105 110
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
 115 120 125
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

<210> 435
 <211> 803
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(780)
 <223> RXA00229

<400> 435
 gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140

 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160

 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175

 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190

 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205

 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220

 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240

 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255

 ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803
 Phe Leu Ser Leu
 260

<210> 436

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15

 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30

 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45

 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60

 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80

 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 Phe Leu Ser Leu
 260

<210> 437

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA02093

<400> 437

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ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc 115
 Met Val Asn Tyr Val
 1 5

gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn
 10 15 20

cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn
 25 30 35

tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
		40					45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
		55				60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
		70			75					80					85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
		135				140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggc	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
		150			155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
		215				220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
		230			235				240					245			
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
			250					255					260				
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctattt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
			265														

<210> 438

<211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 438

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Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
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Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
          20           25           30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
          35           40           45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
          50           55           60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
          65           70           75           80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
          85           90           95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
          100           105           110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
          115           120           125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
          130           135           140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
          145           150           155           160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
          165           170           175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
          180           185           190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
          195           200           205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
          210           215           220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
          225           230           235           240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
          245           250           255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
          260           265
  
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<210> 439
 <211> 951
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXA02791

<400> 439

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ggcgtttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1                               5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10                               15                               20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25                               30                               35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40                               45                               50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55                               60                               65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70                               75                               80                               85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90                               95                               100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105                               110                               115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120                               125                               130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135                               140                               145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150                               155                               160                               165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170                               175                               180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185                               190                               195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210
 gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225
 aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245
 tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260
 atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
 265 270 275
 taagtccccg ccacctctc aac 951

<210> 440

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
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 Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175



Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

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 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(670)
 <223> RXA01699

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 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115
 Met Glu Arg Asn Glu
 1 5
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu
 10 15 20
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys
 25 30 35
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val
 40 45 50
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala
 55 60 65
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile
 70 75 80 85
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly
 90 95 100
 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp
 105 110 115
 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala
 120 125 130
 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His
 135 140 145
 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala
 150 155 160 165
 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala
 170 175 180
 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690
 Ala Val Leu His His Leu Glu Ile Asp
 185 190
 tta 693

<210> 442

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
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 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
 20 25 30
 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
 35 40 45
 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50 55 60
 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65 70 75 80
 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
 85 90 95
 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
 100 105 110
 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
 115 120 125
 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala



130	135	140	
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu			
145	150	155	160
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro			
	165	170	175
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp			
	180	185	190
<210> 443			
<211> 959			
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<221> CDS			
<222> (97) .. (936)			
<223> RXA00952			
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cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114			
		Met Ser Arg Tyr Asp Asp	
		1 5	
ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162			
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe			
	10	15	20
atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210			
Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser			
	25	30	35
aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258			
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe			
	40	45	50
tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306			
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg			
	55	60	65
gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354			
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys			
	75	80	85
cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402			
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr			
	90	95	100
ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450			
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe			
	105	110	115
gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498			
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg			
	120	125	130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro
 135 140 145 150

 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val
 155 160 165

 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val
 170 175 180

 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val
 185 190 195

 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly
 200 205 210

 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser
 215 220 225 230

 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys
 235 240 245

 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu
 250 255 260

 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys
 265 270 275

 aag gtt taggccttta aatgtggcaa tgt 959
 Lys Val
 280

<210> 444

<211> 280

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu
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 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu
 20 25 30

 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu
 35 40 45

 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val
 50 55 60

 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser
 65 70 75 80



Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala
260 265 270

Met Lys Ala Ala Thr Lys Lys Val
275 280

<210> 445
<211> 1237
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1237)
<223> RXN00956

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accatctcca cattccatta ctaaagggtt aaataggatc atg act gaa aaa gaa 115
Met Thr Glu Lys Glu
1 5
aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta
 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446
 <211> 379
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 446
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 20 25 30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85										90					95				
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg				
			100					105						110					
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly				
		115					120					125							
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val				
	130					135					140								
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg				
145					150					155					160				
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly				
				165					170					175					
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr				
			180					185						190					
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro				
		195					200					205							
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala				
210						215					220								
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val				
225					230					235					240				
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe				
				245					250					255					
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu				
			260					265						270					
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile				
		275					280						285						
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly				
	290					295					300								
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly				
305					310					315					320				
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				
				325					330					335					
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala				
			340					345					350						
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala				
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Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val									
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<211> 1231

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1231)

<223> FRXA00956

<400> 447

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 Met Thr Glu Lys Glu
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
 10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
 25 30 35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
 Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
 105 110 115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
 Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
 120 125 130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
 Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
 135 140 145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
 Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
 150 155 160 165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
 185 190 195

tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cg t gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	
gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc gcc	931
Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly	
265 270 275	
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc	979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly	
280 285 290	
acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc	
1027	
Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser	
295 300 305	
tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac	
1075	
Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His	
310 315 320 325	
gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac	
1123	
Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp	
330 335 340	
gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc	
1171	
Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile	
345 350 355	
atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc	
1219	
Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg	
360 365 370	
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1231	
Ala Lys Thr Ala	
375	

<210> 448

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 448



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 20 25 30
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
 85 90 95
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
 100 105 110
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
 115 120 125
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
 130 135 140
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
 145 150 155 160
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
 165 170 175
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
 180 185 190
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
 195 200 205
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
 210 215 220
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
 225 230 235 240
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

325 330 335
 Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala
 340 345 350
 Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala
 355 360 365
 Tyr Ala Leu Lys Arg Ala Lys Thr Ala
 370 375

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 <211> 1401
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(1378)
 <223> RXA00064

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 ggctccgtcta ttttgcacc acatgcggag gtacgcagtt atg agt tca gtt tcg 115
 Met Ser Ser Val Ser
 1 5

 ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163
 Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile
 10 15 20

 aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211
 Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu
 25 30 35

 act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259
 Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu
 40 45 50

 ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307
 Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp
 55 60 65

 gtc cgt aac tat ggc ggc ctg gat ggc atc gtt gat att cgc cag att 355
 Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile
 70 75 80 85

 tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggc gat 403
 Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp
 90 95 100

 gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att 451
 Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile
 105 110 115

 ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt 499
 Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val
 120 125 130

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg 547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr
135 140 145

gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc 595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly
150 155 160 165

cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag 643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys
170 175 180

ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg 691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val
185 190 195

aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg 739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro
200 205 210

gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc 787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr
215 220 225

gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct 835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala
230 235 240 245

ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act 883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr
250 255 260

ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc 931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg
265 270 275

aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag 979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys
280 285 290

gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg
1027
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val
295 300 305

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac
1075
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn
310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg
1123
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala
330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt
1171
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val
345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc
 1219
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag
 1267
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt
 1315
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg
 1363
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
 410 415 420

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 1401
 Glu His Tyr Ala Asn
 425

<210> 450
 <211> 426
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser
 115 120 125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg
 130 135 140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro
 145 150 155 160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys
 165 170 175
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro
 180 185 190
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met
 195 200 205
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala
 210 215 220
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly
 225 230 235 240
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser
 245 250 255
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr
 260 265 270
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly
 275 280 285
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly
 290 295 300
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu
 305 310 315 320
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala
 325 330 335
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile
 340 345 350
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala
 355 360 365
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu
 370 375 380
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro
 385 390 395 400
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val
 405 410 415
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn
 420 425

<210> 451

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN00448

<400> 451

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                                   Val Thr Thr Lys Asp
                                   1                               5
att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
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Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
              25                30                35
cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
              40                45                50
tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
              55                60                65
ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
              70                75                80                85
gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
              90                95                100
gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
              105                110                115
cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
              120                125                130
agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
              135                140                145
ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
              150                155                160                165
atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
              170                175                180
gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
              185                190                195
cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
              200                205                210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
 215 220 225

 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu
 230 235 240 245

 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
 250 255 260

 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
 265 270 275

 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
 280 285 290

 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca
 1027
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
 295 300 305

 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag
 1075
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
 310 315 320 325

 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc
 1120
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 330 335 340

 tagttttatc ggctgatgat tct
 1143

<210> 452

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
 1 5 10 15

 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
 20 25 30

 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45

 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60

 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80

 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe



85					90					95					
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
			100					105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
		130					135					140			
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
				150					155						160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
			165						170					175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
		195					200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
		210					215					220			
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
				225			230					235			240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
				245					250					255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
			260					265					270		
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
		275					280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
		290					295					300			
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
				305			310					315			320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
				325					330					335	
Ile	Glu	Val	Phe												
			340												

<210> 453

<211> 689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(666)

<223> FRXA00448

<400> 453
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Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
1 5 10 15

gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc ttc 96
Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
20 25 30

gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc atc 144
Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
35 40 45

tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt gtc 192
Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
50 55 60

cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct cat 240
Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
65 70 75 80

tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac ggt 288
Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
85 90 95

ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc acc 336
Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
100 105 110

cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa agc 384
Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
115 120 125

aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc ctc 432
Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
130 135 140

cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag caa 480
His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
145 150 155 160

ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc tcc 528
Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
165 170 175

ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca tcc 576
Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
180 185 190

agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag cag 624
Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
195 200 205

ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc 666
Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
210 215 220

tagttttatc ggctgatgat tct 689

<210> 454

<211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 454

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Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
  1                      5                      10                      15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
                20                      25                      30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
                35                      40                      45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
  50                      55                      60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser His
  65                      70                      75                      80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
                85                      90                      95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
                100                      105                      110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
  115                      120                      125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
  130                      135                      140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
  145                      150                      155                      160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
                165                      170                      175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
                180                      185                      190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
  195                      200                      205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
  210                      215                      220

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<210> 455
 <211> 346
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(346)
 <223> FRXA00452

<400> 455
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                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
    70                75                80

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<210> 456

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

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Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
    1                5                10                15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
                20                25                30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
                35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
    50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
    65                70                75                80

Asp Ser

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<210> 457

<211> 1248

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1225)

<223> RXA00584

<400> 457

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agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
                                         Met His Ser Pro Glu
                                         1                               5
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
                        10                               15                               20
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
                        25                               30                               35
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
                        40                               45                               50
gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
                        55                               60                               65
cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
                        70                               75                               80                               85
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
                        90                               95                               100
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
                        105                               110                               115
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
                        120                               125                               130
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
                        135                               140                               145
gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
                        150                               155                               160                               165
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
                        170                               175                               180
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
                        185                               190                               195
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
                        200                               205                               210
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
                        215                               220                               225

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tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa
 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag
 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg
 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc
 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca
 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370

gcc aag taattaaggg cgctagactg tta
 1248
 Ala Lys
 375

<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
 1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45						
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	
50					55					60						
Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	
65					70					75					80	
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	
85					90					95						
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	
100					105					110						
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	
115					120					125						
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	
130					135					140						
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	
145					150					155					160	
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	
165					170					175						
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	
180					185					190						
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	
195					200					205						
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	
210					215					220						
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	
225					230					235					240	
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly	
245					250					255						
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	
260					265					270						
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys	
275					280					285						
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile	
290					295					300						
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu	
305					310					315					320	
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly	
325					330					335						
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp	
340					345					350						
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg	
355					360					365						

Glu Arg Arg Ala Ala Ala Lys
370 375

<210> 459
<211> 1983
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1960)
<223> RXA00579

<400> 459
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gtgcttttct cgttgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115
Met Arg Val Leu Ile
1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
 215 220 225

ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa
 1027
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt
 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct
 1123
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc gcc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala



375	380	385
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat 1315		
Pro Leu Ala Ala Tyr	Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr 395	400 405
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg 1363		
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410	415	420
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro 425	430	435
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu 440	445	450
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu 455	460	465
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro 470	475	480 485
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490	495	500
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505	510	515
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly 520	525	530
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535	540	545
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550	555	560 565
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570	575	580



cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205



Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp
 450 455 460
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
 465 470 475 480
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
 485 490 495
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
 500 505 510
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
 530 535 540
 Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
 545 550 555 560
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
 565 570 575
 Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
 580 585 590
 Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
 595 600 605
 Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
 610 615 620

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 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(724)
 <223> RXA00958

<400> 461
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 ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5
 ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20
 gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35
 gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 50
 cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65
 aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85
 ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100
 ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205
 tca 747

<210> 462

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
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 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
 65 70 75 80
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His



130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200
		205

<210> 463
 <211> 469
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(469)
 <223> RXN03007

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 gaacagcttc tcgcgaacta ataaaaaaag gatttgattc atg act tct cca gca 115
 Met Thr Ser Pro Ala
 1 5
 aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163
 Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu
 10 15 20
 gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211
 Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp
 25 30 35
 gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259
 Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu
 40 45 50
 cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307
 Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala
 55 60 65
 cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355
 Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr
 70 75 80 85
 ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403
 Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu
 90 95 100
 atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451
 Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser

105 110 115 469

gtg agc tcc aag tcc ggc
 Val Ser Ser Lys Ser Gly
 120

<210> 464
 <211> 123
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 464
 Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn
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 Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr
 20 25 30
 Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
 35 40 45
 Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
 50 55 60
 Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu
 65 70 75 80
 Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr
 85 90 95
 Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys
 100 105 110
 His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly
 115 120

<210> 465
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXN02918

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 Met Ser Glu Ile Leu
 1 5
 gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163
 Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala
 10 15 20
 ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211
 Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

25 30 35
 acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc 259
 Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr
 40 45 50
 gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg 307
 Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala
 55 60 65
 cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg 355
 Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu
 70 75 80 85
 ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc 403
 Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser
 90 95 100
 aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc 451
 Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser
 105 110 115
 cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct 499
 Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser
 120 125 130
 gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac 541
 Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp
 135 140 145
 taattgtctc ccatttaagg agt 564

 <210> 466
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 466
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 Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp
 20 25 30
 Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu
 35 40 45
 Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe
 50 55 60
 Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr
 65 70 75 80
 Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg
 85 90 95
 Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys
 100 105 110
 Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp

115 120 125

Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly
 130 135 140

Gln Leu Asp
 145

<210> 467
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXN01116

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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115
 Met Ala Ala Arg Val
 1 5

gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg 163
 Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met
 10 15 20

cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt 211
 Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu
 25 30 35

cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag 259
 His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu
 40 45 50

gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt 307
 Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val
 55 60 65

gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc 355
 Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile
 70 75 80 85

cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc 403
 Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser
 90 95 100

cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag 451
 Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys
 105 110 115

ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc 499
 Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile
 120 125 130

gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag 547
 Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys
 135 140 145

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val
 150 155 160 165
 acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu
 170 175 180
 atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr
 185 190 195
 gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735
 Glu Ala Asp Phe Lys Val Ala
 200

<210> 468

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 468

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 Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
 20 25 30
 Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
 35 40 45
 Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
 50 55 60
 Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
 65 70 75 80
 Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
 85 90 95
 Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 100 105 110
 Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
 115 120 125
 Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
 130 135 140
 Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
 145 150 155 160
 Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
 165 170 175
 Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
 180 185 190
 Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

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<211> 876
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(853)
<223> RXN01115
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Met Ala Ile Leu His 5															
1															
agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163															
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser 20															
10 15															
ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211															
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His 35															
25 30															
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259															
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser 50															
40 45															
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307															
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val 65															
55 60															
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355															
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly 85															
70 75 80															
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403															
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp 100															
90 95															
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451															
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu 115															
105 110 115															
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499															
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr 130															
120 125 130															
ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547															
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp 145															
135 140 145															
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595															
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala 165															
150 155 160 165															
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643															

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr
 170 175 180
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr
 185 190 195
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile
 200 205 210
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro
 215 220 225
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu
 230 235 240 245
 cta gca cag cat ttc gct taatgttgta ggcatgttca caa 876
 Leu Ala Gln His Phe Ala
 250

<210> 470

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

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 1 5 10 15
 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln
 20 25 30
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
 35 40 45
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
 50 55 60
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
 65 70 75 80
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
 85 90 95
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
 100 105 110
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
 115 120 125
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
 130 135 140
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
 145 150 155 160
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys



165	170	175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr 180	185	190
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro 195	200	205
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala 210	215	220
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn 225	230	235
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala 245	250	

<210> 471
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1261)
 <223> RXS00116

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 Met Ser Asn Asp Phe
 1 5
 gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
 10 15 20
 acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
 25 30 35
 cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
 Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
 40 45 50
 att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
 Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
 55 60 65
 ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
 Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
 70 75 80 85
 tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
 Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
 90 95 100
 att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
 Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

105										110					115					
gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499				
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala					
		120						125					130							
ggg	gcg	acg	cgg	gtg	gcg	gtt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547				
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp					
	135					140					145									
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595				
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg					
150					155					160					165					
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643				
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser					
				170					175					180						
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691				
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu					
		185						190					195							
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739				
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln					
	200						205					210								
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787				
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val					
	215					220					225									
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835				
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr					
230				235						240				245						
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883				
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala					
			250					255					260							
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931				
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val					
			265					270					275							
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979				
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys					
		280					285					290								
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg	1027				
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala					
	295					300					305									
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat	1075				
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp					
310					315					320				325						
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag	1123				
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys					
				330					335				340							

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
 1261
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
 375 380 385

tagtttgaac aggttggttg ggg
 1284

<210> 472
 <211> 387
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
 20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
 35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
 85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
 100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190



Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
 385

<210> 473
 <211> 607
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(607)
 <223> FRXA00116

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 ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
 Met Thr Gln Arg Ala
 1 5
 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80



Ala	Ile	Thr	Ala	Thr 85	Val	Leu	Gly	Leu	Val 90	Glu	Pro	Gly	Asp	Glu 95	Val
Ile	Val	Leu	Glu 100	Pro	Tyr	Tyr	Asp	Ala 105	Tyr	Ala	Ala	Ala	Ile 110	Ala	Leu
Ala	Gly	Ala 115	Thr	Arg	Val	Ala	Val 120	Pro	Leu	Gln	Glu	Val 125	Glu	Asn	Ser
Trp	Asp 130	Val	Asp	Val	Asp	Lys 135	Leu	His	Ala	Ala	Val 140	Thr	Lys	Lys	Thr
Arg 145	Met	Ile	Ile	Val	Asn 150	Ser	Pro	His	Asn	Pro 155	Thr	Gly	Ser	Val	Phe 160
Ser	Lys	Lys	Ala	Leu 165	Lys	Gln	Leu	Ala							

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<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(820)  
<223> RXS00391
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<div> <div>Leu</div> <div>Leu</div> <div>Arg</div> <div>Asp</div> <div>Ser</div> </div> <div>15</div>															5
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc															163
<div>Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala</div> <div>101520</div>															
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg															211
<div>Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu</div> <div>253035</div>															
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa															259
<div>Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu</div> <div>404550</div>															
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag															307
<div>Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln</div> <div>556065</div>															
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat															355
<div>Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp</div> <div>70758085</div>															
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa															403
<div>Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu</div> <div>9095100</div>															

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

 tgc 843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

 Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85										90					95				
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser				
			100					105					110						
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile				
		115					120					125							
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu				
	130					135					140								
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val				
145					150					155					160				
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly				
				165					170					175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu				
			180					185					190						
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His				
		195					200					205							
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu				
	210					215					220								
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His				
225					230					235					240				

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXS00393

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 aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	



gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 478
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478
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 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp



260 265 270
 Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
 275 280 285
 Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
 290 295

 <210> 479
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(982)
 <223> FRXA00393

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 aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5

 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20

 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35

 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65

 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85

 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

 gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115

 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130

 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

cat tagcggttag ctaaaacgct ttt
 1005
 His

<210> 480
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 480
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285
 Cys Ser Arg Ala Trp His
 290

<210> 481

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXS00446

<400> 481

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 ggtgacggag gctacttggg gggctaatacg gtacccggat atg ggt gcg gtt gag 115
 Met Gly Ala Val Glu

1															5		
ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
			10						15					20			
acg	gta	ggc	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211	
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
			25					30					35				
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
		40					45					50					
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307	
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
	55					60					65						
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355	
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
	70				75					80					85		
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403	
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
				90					95					100			
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451	
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
			105					110					115				
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499	
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe		
		120					125					130					
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547	
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
		135				140					145						
gac	aac	gtg	att	ggc	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595	
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
	150				155					160				165			
ggc	ttg	cgt	gtt	ggc	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643	
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
			170					175						180			
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691	
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala		
			185					190					195				
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739	
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val		
		200					205					210					
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggc	gct	787	
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala		
		215				220					225						
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835	
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala		
	230				235					240					245		

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260
 ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275
 ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285
 tgc 987

<210> 482
 <211> 288
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 482
 Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
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 Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30
 Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45
 Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60
 Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80
 Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95
 Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110
 Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125
 Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 483
 <211> 545
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(522)
 <223> FRXA00446

<400> 483
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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15
 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125



ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

tagtcctttgg cgttttgcgg tgc 545

<210> 484

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 485

<211> 1230

<212> DNA

<213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1207)
 <223> RXS00618

<400> 485
 gctgcattag agggctcgat ctcgatctaa aagcagtacg cagataggct tgtctcttat 60
 gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac 115
 Met Gln Met Leu Asp
 1 5
 cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20
 gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35
 gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50
 gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65
 gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85
 ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
 90 95 100
 gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
 Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
 105 110 115
 tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
 Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
 120 125 130
 ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
 Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
 135 140 145
 gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
 Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
 150 155 160 165
 ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
 Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
 170 175 180
 gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
 Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
 185 190 195
 ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
 200 205 210
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
 215 220 225
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
 1027
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365
 taggttagtt tcg
 1230

<210> 486

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1 5 10 15



Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340 345 350
 Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365
 Lys

 <210> 487
 <211> 657
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(634)
 <223> FRXA00618

 <400> 487
 cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcgatga 60
 caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

 ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

 acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35

 atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50

 ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55 60 65

 ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70 75 80 85

 cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90 95 100

 ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
 105 110 115

 tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
 120 125 130

 gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 489
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 gaagccaagc actagaagca atgttcagcc gtttcgctgc atg cag atg ttg gac 115
 Met Gln Met Leu Asp
 1 5
 cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20
 gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35
 gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50
 gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65
 gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85
 ggt gga ttc gtg gca tcg ttt atc gcc acc 385
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 90 95

<210> 490
 <211> 95
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 490
 Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1 5 10 15
 Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 85 90 95

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<220>
<221> CDS
<222> (101)..(1198)
<223> RXS01105
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707

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Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
1027
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
1075
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
1123
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
1171
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
1218
Ala Ala Glu Ile Ile Lys Leu Asn Leu
360 365

tga
1221

<210> 492
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 492

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 Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
 20 25 30
 Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
 35 40 45
 Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50 55 60
 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65 70 75 80
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
 85 90 95
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
 100 105 110
 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
 115 120 125
 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
 130 135 140
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
 145 150 155 160
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
 165 170 175
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
 180 185 190
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
 195 200 205
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
 210 215 220
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
 225 230 235 240
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
 245 250 255
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
 260 265 270
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320

Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
355 360 365

<210> 493

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1729)

<223> RXS02315

<400> 493

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gaatcgtatc cgtacctgga gacgatctag actgttgtgc atg tcc agc acg cca 115
Met Ser Ser Thr Pro
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat caq gta gcg caq att gct gaa agc ctt gct cag ggg 547

Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
 135 140 145
 gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
 Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
 150 155 160 165
 gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
 Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
 170 175 180
 tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
 Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
 185 190 195
 gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739
 Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly
 200 205 210
 ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787
 Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr
 215 220 225
 aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835
 Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val
 230 235 240 245
 tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883
 Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val
 250 255 260
 gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931
 Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp
 265 270 275
 cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979
 Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp
 280 285 290
 ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc
 1027
 Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly
 295 300 305
 acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt
 1075
 Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu
 310 315 320 325
 gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc
 1123
 Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe
 330 335 340
 acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc
 1171
 Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly
 345 350 355
 gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg
 1219

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala
 410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 494
 <211> 543
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 494

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Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
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Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
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Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35          40          45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
          50          55          60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65          70          75          80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85          90          95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
          115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
          210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
          275          280          285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290                               295                               300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
305                               310                               315                               320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
                               325                               330                               335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
                               340                               345                               350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355                               360                               365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370                               375                               380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
385                               390                               395                               400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
                               405                               410                               415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
 420                               425                               430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435                               440                               445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450                               455                               460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
465                               470                               475                               480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
                               485                               490                               495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
                               500                               505                               510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515                               520                               525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530                               535                               540

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<210> 495

<211> 1434

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1411)

<223> RXS02550

<400> 495

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tagcttttcaa ctacgcacac aaagtggcaa cattgagcgg	gtg Val 1	act Thr	aca Thr	gac Asp	aag Lys 5	115
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg						163
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala						
	10				20	
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat						211
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp						
	25				35	
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg						259
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val						
	40				50	
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag						307
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys						
	55				65	
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg						355
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val						
	70				80	85
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc						403
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser						
	90				95	100
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac						451
Thr Ser Lys Gly Ile Ile Pro Ala Arg Ala Val Val Thr Arg Tyr						
	105				110	115
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta						499
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu						
	120				125	130
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc						547
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Gln Ala Leu Leu						
	135				140	145
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg						595
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp						
	150				155	160
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt						643
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys						
	170				175	180
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa						691
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys						
	185				190	195
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc						739
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro						
	200				205	210
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att						787
Thr Gly Ala Val Tyr Pro Arg Val Leu Glu Gln Ile Val Glu Ile						
	215				220	225

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
 425 430 435

tagtagttgt taggattcac cac
1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn
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Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr
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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
260 265 270

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430
 Ser Thr Tyr Lys Gln
 435

<210> 497

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1057)

<223> RXS02319

<400> 497

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 Met Ser Asn Tyr Ser
 1 5
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
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 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
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 1080

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 <213> Corynebacterium glutamicum

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 35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
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Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140 -

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210 215 220
 Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
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 Leu Lys Leu His Pro
 1 5
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
 10 15 20
 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
 25 30 35
 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
 40 45 50
 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
 55 60 65
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
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 ctg ttt tagtcttcat tcttgctggc tgc 384
 Leu Phe



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<210> 500
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
          20                25              30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
      35                40              45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
    50                55              60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
  65                70              75            80
Arg Ala Ile Ala Lys Leu Phe
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<213> Corynebacterium glutamicum
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						Met Thr Ser Arg Thr										
						1 5										
ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc	163															
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser																
10 15 20																
gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct																211
Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser																
25 30 35																
gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg																259
Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu																
40 45 50																
gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg																307
Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro																
55 60 65																
gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg																355

Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
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 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
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 215 220 225

<210> 502

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 502

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 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80



Arg	Arg	Tyr	Asn	Met	Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val		
				85					90							95	
Val	Gly	Thr	Lys	Glu	Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile		
			100					105					110				
Ser	Gly	Thr	Val	Val	Ile	Pro	Glu	Ile	Ala	Tyr	Pro	Thr	Tyr	Glu	Val		
		115					120					125					
Ala	Val	Val	Ala	Ala	Gly	Cys	Thr	Val	Leu	Arg	Ser	Asp	Ser	Leu	Phe		
	130					135					140						
Lys	Leu	Gly	Pro	Gln	Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser		
	145				150					155					160		
Asn	Pro	Thr	Gly	Lys	Val	Leu	Gly	Ile	Pro	His	Leu	Arg	Lys	Val	Val		
				165					170					175			
Lys	Trp	Ala	Gln	Glu	Asn	Asn	Val	Ile	Leu	Ala	Ala	Asp	Glu	Cys	Tyr		
			180					185					190				
Leu	Gly	Leu	Gly	Trp	Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp		
		195					200					205					
Pro	Arg	Val	Cys	Asp	Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser		
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Leu																	
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Met Pro Gly Lys Ile 5																	
ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163																	
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro 20																	
gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211																	
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr 25 30 35																	
gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259																	
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn 40 45 50																	
cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307																	

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85
 ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504
 <211> 89
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
 20 25 30
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80
 Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 505
 <211> 621
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(598)
 <223> RXS03074

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 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35



ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

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<210> 506

<211> 166

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 506

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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
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Glu Ala Pro Ile Lys Gln
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<210> 507

<211> 3075

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(3052)

<223> RXC01434

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 Val Leu Gly Ala Val
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ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
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 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
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 90 95 100

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 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
 105 110 115

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Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
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Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
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Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
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Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	
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310 315 320 325	
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	
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330 335 340	

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 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta
 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
 1507
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
 1555
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag
 1603
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc
 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg
 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat
 1747
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
 1795
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc
 1843
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
 1891
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
 615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
 2035
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
 2131
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
 2179
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
 2275
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat
 2899
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
 920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
 2947
 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
 935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
 2995
 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
 950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
 3043
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
 970 975 980

ggt ggt tgg taaattacgc gttgtgatt gac
 3075
 Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 508

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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
 20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160



Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480



Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

805										810					815				
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser				
			820					825					830						
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln				
		835					840					845							
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr				
	850					855					860								
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu				
865					870				875						880				
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr				
				885					890					895					
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr				
			900					905					910						
Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile				
		915					920					925							
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp				
930						935					940								
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp				
945					950				955						960				
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile				
				965					970					975					
Ala	Glu	Val	Gln	Leu	Val	Gly	Trp												
				980															

<210> 509

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXC02080

<400> 509

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tttgtcctgt	tgcttattgt	gcaggaattc	ggaggcggac	atg	tca	atc	gag	tgg	115
				Met	Ser	Ile	Glu	Trp	
				1				5	

tta	caa	att	gtt	gaa	tta	gga	gcg	atc	ttt	ggt	gca	ggt	ttc	ctc	gca	163
Leu	Gln	Ile	Val	Glu	Leu	Gly	Ala	Ile	Phe	Gly	Ala	Gly	Phe	Leu	Ala	
			10					15						20		

gga	agc	atc	aat	gta	att	gtc	gga	gca	gga	aca	tta	gtg	tcg	ttt	cct	211
Gly	Ser	Ile	Asn	Val	Ile	Val	Gly	Ala	Gly	Thr	Leu	Val	Ser	Phe	Pro	
			25				30						35			

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

<210> 510
 <211> 269
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510

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Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
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Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
          20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
          35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
 50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
          85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
          100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
          115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
          130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
          145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
          165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
          180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
          195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
          210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
          225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
          245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
          260          265

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 <211> 669
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXC02789

<400> 511

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ttcttaacac	taaacaatgg	aaaggtaagc	gggtttttct	atg	aag	ggt	tcc	gcc	115
				Met	Lys	Val	Ser	Ala	
				1				5	

gat	aca	ccc	ggt	cac	gat	gat	cca	ggc	cca	ggc	cgg	cgc	ctt	ggc	tta	163
Asp	Thr	Pro	Gly	His	Asp	Asp	Pro	Gly	Pro	Gly	Arg	Arg	Leu	Gly	Leu	
				10				15					20			

gat	gtc	ggc	acc	gtg	cgc	atc	gga	gtg	gca	gcc	tct	gac	cgc	gat	gcc	211
Asp	Val	Gly	Thr	Val	Arg	Ile	Gly	Val	Ala	Ala	Ser	Asp	Arg	Asp	Ala	
			25				30					35				

aag	ctt	gcc	atg	cct	gtg	gaa	acc	gtt	ccg	cgg	gaa	act	gga	ttc	aaa	259
Lys	Leu	Ala	Met	Pro	Val	Glu	Thr	Val	Pro	Arg	Glu	Thr	Gly	Phe	Lys	
		40				45					50					

ggg	cca	gac	ctg	gcc	gat	att	gat	cgg	ttg	gtc	gcc	atc	ggt	gag	gaa	307
Gly	Pro	Asp	Leu	Ala	Asp	Ile	Asp	Arg	Leu	Val	Ala	Ile	Val	Glu	Glu	
	55					60					65					

tac	aac	gcc	gtg	gaa	gtc	att	gtt	ggt	cta	ccc	aca	gat	ctg	cag	gga	355
Tyr	Asn	Ala	Val	Glu	Val	Ile	Val	Gly	Leu	Pro	Thr	Asp	Leu	Gln	Gly	
70				75					80					85		

aat	ggc	tcc	gcc	agt	gtg	aag	cat	gca	aag	gaa	att	gct	ttc	cgc	gtc	403
Asn	Gly	Ser	Ala	Ser	Val	Lys	His	Ala	Lys	Glu	Ile	Ala	Phe	Arg	Val	
			90						95				100			

cgt	cgg	cgc	ctc	acc	aat	gct	gga	aag	aac	att	ccg	gta	cgg	ctt	ggc	451
Arg	Arg	Arg	Leu	Thr	Asn	Ala	Gly	Lys	Asn	Ile	Pro	Val	Arg	Leu	Gly	
			105				110						115			

gac	gaa	cgc	ctc	acc	acc	gtc	gtg	gcc	acc	caa	gcc	ttg	cgg	gcc	tca	499
Asp	Glu	Arg	Leu	Thr	Thr	Val	Val	Ala	Thr	Gln	Ala	Leu	Arg	Ala	Ser	
		120				125						130				

gga	gtc	agc	gaa	aaa	gcg	gga	cgt	aaa	gtt	att	gat	caa	gct	gcc	gca	547
Gly	Val	Ser	Glu	Lys	Ala	Gly	Arg	Lys	Val	Ile	Asp	Gln	Ala	Ala	Ala	
	135					140					145					

gta	gaa	atc	ctt	caa	acc	tgg	ttg	gat	gct	cgc	acc	cga	gcc	ctt	gaa	595
Val	Glu	Ile	Leu	Gln	Thr	Trp	Leu	Asp	Ala	Arg	Thr	Arg	Ala	Leu	Glu	
150				155					160					165		

cca	caa	tcc	aca	gac	acc	caa	gat	ttc	gac	gag	aag	gga	aat	ttc	cca	643
Pro	Gln	Ser	Thr	Asp	Thr	Gln	Asp	Phe	Asp	Glu	Lys	Gly	Asn	Phe	Pro	
				170				175					180			

gga	tgaaccaa	at	ccgaaaccgc	cgg	669
Gly					

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<210> 512
<211> 182
<212> PRT
<213> Corynebacterium glutamicum
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<400> 512

Met Lys Val Ser Ala Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly
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Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
20 25 30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
35 40 45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
50 55 60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
65 70 75 80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
85 90 95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
100 105 110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
115 120 125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
130 135 140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
145 150 155 160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
165 170 175

Lys Gly Asn Phe Pro Gly
180

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<210> 513
<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101) . . (880)

<223> RXC02295

<400> 513

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gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
1 5

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga	163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg	211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa	499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc	643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg	787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt	835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg	880
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met	
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<212> PRT
<213> Corynebacterium glutamicum
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Val	Leu	Ile	Pro	Leu	Ile	Leu	Ala	Val	Met	Pro	Gln	Leu	Ala	Pro	Val	
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Thr	Ala	Leu	Ala	Ser	Asn	Lys	Leu	Ala	Ala	Val	Thr	Gly	Thr	Ala	Ser	
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Ala	Ala	Phe	Thr	Leu	Val	Arg	Arg	Val	Lys	Pro	Asp	Lys	Lys	Leu	Leu	
65					70					75					80	
Ala	Leu	Tyr	Val	Leu	Val	Ala	Ala	Val	Cys	Ser	Gly	Ala	Gly	Ala	Leu	
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Ala	Ala	Ser	Leu	Ile	Asp	Lys	Gln	Ile	Met	Arg	Pro	Leu	Ile	Ile	Val	
			100					105					110			
Leu	Met	Leu	Val	Val	Gly	Leu	Ile	Val	Val	Phe	Lys	Pro	Asn	Phe	Gly	
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Thr	Gly	Glu	Ser	Lys	Ala	Leu	Pro	Thr	Gly	Trp	Lys	Arg	Trp	Ala	Ala	
	130					135					140					
Ile	Val	Ala	Val	Gly	Leu	Ile	Ala	Ala	Tyr	Asp	Gly	Ile	Phe	Gly	Pro	
145					150					155					160	
Gly	Thr	Gly	Met	Phe	Leu	Ile	Met	Ala	Phe	Thr	Ala	Leu	Leu	Ser	Gln	
				165					170					175		
Asn	Phe	Leu	Ser	Ser	Ala	Ala	Met	Ala	Lys	Val	Val	Asn	Thr	Ala	Thr	
			180					185					190			
Asn	Leu	Gly	Ala	Leu	Ile	Val	Phe	Ile	Ile	Gly	Gly	His	Met	Trp	Trp	
		195					200					205				
Thr	Leu	Gly	Leu	Val	Leu	Ala	Val	Ala	Asn	Val	Ala	Gly	Ala	Gln	Leu	
	210					215					220					
Gly	Ala	Arg	Thr	Val	Leu	Gly	Gly	Gly	Thr	Arg	Leu	Ile	Arg	Tyr	Ala	
225					230					235					240	
Leu	Leu	Thr	Leu	Val	Val	Val	Met	Ser	Val	Tyr	Leu	Thr	Trp	Gln	Gln	
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Ile Gln Gly Met
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<213> Corynebacterium glutamicum

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<222> (101)..(1132)
<223> RXN03063

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Val Glu Asp Leu Ser
1 5
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro
10 15 20
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
25 30 35
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
40 45 50
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
55 60 65
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val
70 75 80 85
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
90 95 100
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
105 110 115
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
120 125 130
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
135 140 145
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
150 155 160 165

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
 280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc
 1027
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
 295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc
 1075
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
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<210> 516

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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 35 40 45
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp
 50 55 60
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala
 65 70 75 80
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys
 85 90 95
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu
 100 105 110
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn
 115 120 125
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr
 130 135 140
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg
 145 150 155 160
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser
 165 170 175
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr
 180 185 190
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile
 195 200 205
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val
 210 215 220
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly
 225 230 235 240
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe
 245 250 255
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe
 260 265 270
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys
 275 280 285
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu
 290 295 300
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly
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<210> 517

<211> 1491

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1468)

<223> RXN02970

<400> 517

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                                         Leu Ala Leu Lys Gly
                                         1           5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10                        15                        20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25                        30                        35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40                        45                        50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55                        60                        65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                        70                        75                        80                        85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90                        95                        100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105                        110                        115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120                        125                        130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135                        140                        145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150                        155                        160                        165

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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
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Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
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1267 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

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 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

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 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450

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 Ala Leu Phe
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<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

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 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145		150		155		160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg						
		165		170		175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro						
		180		185		190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys						
		195		200		205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala						
		210		215		220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly						
		225		230		235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys						
		245		250		255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe						
		260		265		270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe						
		275		280		285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala						
		290		295		300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly						
		305		310		315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala						
		325		330		335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile						
		340		345		350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu						
		355		360		365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile						
		370		375		380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala						
		385		390		395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser						
		405		410		415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu						
		420		425		430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu						
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Leu Thr Phe Ala Gly Ala Leu Phe						
		450		455		

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1330)
 <223> FRXA01009

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 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145
 cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165
 tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180
 acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggt	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	215					220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240					245		
gca	ggt	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250					255					260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gcc	aag	ggt	gtt	aac	gca	ggt	tac	gcc	cca	ctc	ggt	ggc	atc		
1027																	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcc		
1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320					325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
				330					335					340			
gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
1171																	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		
			345					350					355				
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
	375					380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggt	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395					400					405		



ttc aag gaa cgc ggc
1330
Phe Lys Glu Arg Gly
410

<210> 520
<211> 410
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 520
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30
Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45
Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60
Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80
His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95
Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110
Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210 215 220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
225 230 235 240
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
245 250 255

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<210> 521
<211> 1998
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1975)  
<223> RXA01551
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752

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55						60					65					
gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr	
70					75					80					85	
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu	
				90					95					100		
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu	
			105					110					115			
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggg	caa	gct	499
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala	
			120				125					130				
tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro	
	135					140					145					
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
150					155					160					165	
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
				170					175					180		
gtg	cgc	tct	gag	gtg	gcg	cgc	ggg	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185					190					195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggg	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
	215					220					225					
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggg	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
230					235					240				245		
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
				250					255					260		
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
			265					270					275			
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
		280					285					290				
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	
1027																

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met
 295 300 305
 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt
 1075
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg
 310 315 320 325
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg
 1123
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp
 330 335 340
 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag
 1171
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu
 345 350 355
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat
 1219
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp
 360 365 370
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc
 1267
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe
 375 380 385
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac
 1315
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr
 390 395 400 405
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg
 1363
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met
 410 415 420
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct
 1411
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro
 425 430 435
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac
 1459
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp
 440 445 450
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc
 1507
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr
 455 460 465
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac
 1555
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn
 470 475 480 485
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac
 1603
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490	495	500
gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac 1651		
Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp 505 510 515		
gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg 1699		
Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala 520 525 530		
ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg 1747		
Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu 535 540 545		
ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg 1795		
Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro 550 555 560 565		
aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc 1843		
Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly 570 575 580		
gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt 1891		
Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser 585 590 595		
gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg 1939		
Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg 600 605 610		
gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc 1985		
Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg 615 620 625		
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<210> 522

<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

Leu Lys Ala Val Pro Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu 1 5 10 15
Ile Ala Ala Arg Ala Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys 20 25 30
Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu
 50 55 60
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe
 65 70 75 80
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu
 85 90 95
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr
 100 105 110
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met
 115 120 125
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro
 130 135 140
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg
 145 150 155 160
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His
 165 170 175
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile
 180 185 190
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly
 195 200 205
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val
 210 215 220
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg
 225 230 235 240
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His
 245 250 255
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr
 260 265 270
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp
 275 280 285
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln
 290 295 300
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile
 305 310 315 320
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser
 325 330 335
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr
 340 345 350
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala
 355 360 365
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp Ala Ala Gln Phe	Ala Glu Leu Lys Thr	Ile Gly Glu Leu Thr Gln
385	390	395 400
Arg Ala Trp Glu Tyr	Asp Val Gln Val Met	Val Glu Gly Pro Gly His
	405	410 415
Val Pro Leu Asn Met	Ile Gln Glu Asn Asn	Glu Leu Glu Gln Lys Trp
	420	425 430
Ala Ala Asp Ala Pro	Phe Tyr Thr Leu Gly	Pro Leu Val Thr Asp Ile
	435	440 445
Ala Pro Gly Tyr Asp	His Ile Thr Ser Ala	Ile Gly Ala Ala His Ile
	450	455 460
Ala Met Gly Gly Thr	Ala Met Leu Cys Tyr	Val Thr Pro Lys Glu His
	465	470 475 480
Leu Gly Leu Pro Asn	Arg Asp Asp Val Lys	Thr Gly Val Ile Thr Tyr
	485	490 495
Lys Leu Ala Ala His	Ala Ala Asp Val Ala	Lys Gly His Pro Gly Ala
	500	505 510
Arg Ala Trp Asp Asp	Ala Met Ser Lys Ala	Arg Phe Glu Phe Arg Trp
	515	520 525
Asn Asp Gln Phe Ala	Leu Ser Leu Asp Pro	Asp Thr Ala Ile Ala Tyr
	530	535 540
His Asp Glu Thr Leu	Pro Ala Glu Pro Ala	Lys Thr Ala His Phe Cys
	545	550 555 560
Ser Met Cys Gly Pro	Lys Phe Cys Ser Met	Arg Ile Ser Gln Asp Ile
	565	570 575
Arg Asp Met Phe Gly	Asp Gln Ile Ala Glu	Leu Gly Met Pro Gly Val
	580	585 590
Gly Asp Ser Ser Ser	Ala Val Ala Ser Ser	Gly Ala Arg Glu Gly Met
	595	600 605
Ala Glu Lys Ser Arg	Glu Phe Ile Ala Gly	Gly Ala Glu Val Tyr Arg
	610	615 620
Arg		
625		

<210> 523

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> RXA01019

<400> 523

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Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro	
1 5 10 15	
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
50 55 60	
ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
180 185 190	
cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg
 1010
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

aat
 1013

<210> 524

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 524

Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
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Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
 20 25 30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140



Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

<210> 525
 <211> 706
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(706)
 <223> RXA01352

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 ctgggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
 Val Phe Glu Asn Arg
 1 5
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
 10 15 20
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

<210> 526

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala			
1	5	10	15
Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly			
20	25	30	
Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala			
35	40	45	

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp
195 200

<210> 527

<211> 944

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

<400> 527

tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac 48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
1 5 10 15

att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
20 25 30

cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
35 40 45

gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
50 55 60

tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288			
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
85	90	95		
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336			
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
100	105	110		
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384			
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
115	120	125		
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432			
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
130	135	140		
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480			
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
145	150	155	160	
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528			
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
165	170	175		
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576			
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser				
180	185	190		
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624			
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
195	200	205		
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672			
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
210	215	220		
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720			
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
225	230	235	240	
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768			
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
245	250	255		
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816			
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
260	265	270		
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	864			
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
275	280	285		
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	912			
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
290	295	300		
aac gcg ctg tagctgtcaa tttaagaggc cag	944			
Asn Ala Leu				
305				



<210> 528

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
 290 295 300

Asn Ala Leu
 305

<210> 529
 <211> 259
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(259)
 <223> RXA01360

<400> 529
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 gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115
 Met Leu His Ile Ala
 1 5
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 530
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
 1 5 10 15
 Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala
 20 25 30
 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45
 Thr Ser Ser Gly Glu
 50

<210> 531
 <211> 629
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXA01361

<400> 531

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gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg      48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
  1                      5                      10                      15

acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg      96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
                20                      25                      30

gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg      144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
                35                      40                      45

aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc      192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
                50                      55                      60

gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt      240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
        65                      70                      75                      80

gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc      288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
                85                      90                      95

gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc      336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
                100                      105                      110

gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att      384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
                115                      120                      125

gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc      432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
        130                      135                      140

ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg      480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
        145                      150                      155                      160

tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca      528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
                165                      170                      175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt      576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
                180                      185                      190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga      626
Asp Val Cys Asp Pro Phe Arg His Gln Ile
        195                      200

tta                                                                    629

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<210> 532
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 532
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
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 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190
 Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA01208

<400> 533
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 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

	Val	Ala	Asn	Ser	Phe	
	1				5	
ttg gat tct tta act ctt gtt cga caa aac act ccc ctt gtt cag tgt 163						
Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr Pro Leu Val Gln Cys						
			10		15	20
ttg acc aac tct gtg gtc atg caa ttc acg gcc aat gtg ttg ctt gcc 211						
Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala Asn Val Leu Leu Ala			25		30	35
gcg ggt gcg acc cct gcg atg gtg gat act cca gct gaa tcg gca gaa 259						
Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro Ala Glu Ser Ala Glu			40		45	50
ttc gcc gct gtg gcc aat gga gtg ctc atc aat gcg gga act cct tct 307						
Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn Ala Gly Thr Pro Ser			55		60	65
gcg gag caa tac caa ggc atg acc aag gcc att gag ggt gca cga aaa 355						
Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile Glu Gly Ala Arg Lys			70		75	80
						85
gct ggc aca cca tgg gtg tta gac cca gtt gct gtg ggt ggg ttg tcg 403						
Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala Val Gly Gly Leu Ser			90		95	100
gag agg acc aag tat gcg gag gga atc gtc gat aag cag cct gcc gca 451						
Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp Lys Gln Pro Ala Ala			105		110	115
att cgt gga aac gcc tca gag gtc gtg gcg ctt gcg ggg ctc ggt gcc 499						
Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu Ala Gly Leu Gly Ala			120		125	130
ggt ggg cgc ggc gta gac gcg acc gat tcc gtg gaa gtg gcg ttg gag 547						
Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val Glu Val Ala Leu Glu			135		140	145
gcg gcg caa ttg ttg gcc aag cgc act ggt ggc gtc gtg gct gtc tct 595						
Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly Val Val Ala Val Ser			150		155	160
						165
ggt gcg gag gac ttg att gtg tct gcg gat cgg gtg acg tgg ttg cgt 643						
Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg Val Thr Trp Leu Arg			170		175	180
tcg ggg gat ccg atg ttg cag ctg gtg att ggc act gga tgc tct ttg 691						
Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly Thr Gly Cys Ser Leu			185		190	195
ggc gcg ctg aca gct gca tat cta ggc gcc acg gtt gac tca gat att 739						
Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr Val Asp Ser Asp Ile			200		205	210
tcc gcg cac gat gct gtg ttg gct gcg cat gcc cat gtg ggt gct gct 787						
Ser Ala His Asp Ala Val Leu Ala Ala His Ala His Val Gly Ala Ala			215		220	225
ggc cag att gca gca cag aag gca tcg gcg cca ggc agc ttt gcg gtg 835						
Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro Gly Ser Phe Ala Val						

230 235 240 245
 gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser
 250 255 260

 ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927
 Leu Val Asp Val Arg Glu Ala
 265

 <210> 534
 <211> 268
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 534
 Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr
 1 5 10 15

 Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala
 20 25 30

 Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro
 35 40 45

 Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn
 50 55 60

 Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile
 65 70 75 80

 Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala
 85 90 95

 Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp
 100 105 110

 Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu
 115 120 125

 Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val
 130 135 140

 Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly
 145 150 155 160

 Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg
 165 170 175

 Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly
 180 185 190

 Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr
 195 200 205

 Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala
 210 215 220

 His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro
 225 230 235 240



Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala
245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala
260 265

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<210> 535
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1000)
<223> RXA00838
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<400> 535
tcgtctaata gtgctgccaa tccaccggcc attgatgact ccttttgtaga gaaggggtag 60
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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
Met Lys Ile Ala Ile
1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr
 40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp
55 60 65

gta	gtg	atg	att	gct	act	aaa	gca	tta	tcg	cgg	tct	tta	gat	ctc	gct	355
Val	Val	Met	Ile	Ala	Thr	Lys	Ala	Leu	Ser	Arg	Ser	Leu	Asp	Leu	Ala	
70					75					80					85	

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln
90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp
105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro
120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp
135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg
 1023
 Lys Glu Glu Glu Asn Ser Leu
 295 300

<210> 536

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
 1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
 20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
 35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
 50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

<210> 537

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02400

<400> 537

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ttaaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115

Met Ser Ile Ser Arg
1 5

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acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
          10          15          20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
          25          30          35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
          40          45          50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
          55          60          65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
          70          75          80          85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
          90          95          100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
          105          110          115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
          120          125          130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
          135          140          145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
          150          155          160          165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
          170          175          180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
          185          190

tca 693

<210> 538
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<212> PRT
<213> Corynebacterium glutamicum

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			20				25						30			
Val	Gln	Arg	Thr	Asn	Glu	Ile	Leu	Thr	Thr	Ser	Gln	Asn	Pro	Thr	Ser	
			35				40						45			
Ala	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ala	Thr	Thr	Thr	Ser	Ser	Ala	Pro	
			50				55						60			
Val	Glu	Glu	Asp	Val	Glu	Ile	Val	Val	Ser	Pro	Ala	Ala	Leu	Val	Asp	
			65				70						75	80		
Gly	Glu	Gln	Val	Thr	Phe	Glu	Ile	Ser	Gly	Leu	Asp	Pro	Glu	Gly	Gly	
			85						90						95	
Tyr	Tyr	Ala	Ala	Ile	Cys	Asp	Ser	Val	Ala	Asn	Pro	Gly	Asn	Pro	Val	
			100						105						110	
Pro	Ser	Cys	Thr	Gly	Glu	Met	Ala	Asp	Phe	Thr	Ser	Gln	Ala	Trp	Leu	
			115						120						125	
Ser	Asn	Ser	Gln	Pro	Gly	Ala	Thr	Val	Glu	Ile	Ala	Glu	Asp	Gly	Thr	
			130						135						140	
Ala	Thr	Val	Glu	Leu	Glu	Ala	Thr	Ala	Thr	Gly	Thr	Gly	Leu	Asp	Cys	
			145						150						155	160
Thr	Thr	Gln	Ala	Cys	Val	Ala	Lys	Val	Phe	Gly	Asp	His	Thr	Glu	Gly	
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Phe	Arg	Asp	Val	Ala	Glu	Val	Pro	Val	Thr	Phe	Ala	Ala	Ala			
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<210> 539
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (1528)
<223> RXN01209
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Met Cys Glu Arg Pro
1 5
gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20
ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

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40	45	50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala 55 60 65			307
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120 125 130			499
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185 190 195			691
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
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 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528
 Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 540
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 540

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			20					25					30		
Val	Asp	Ser	Ala	Ile	Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp
		35					40					45			
Lys	Asn	Ser	Gly	Val	Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys
	50					55					60				
Glu	Leu	Cys	Asp	Ala	Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu
65					70					75					80
Asp	Ile	Ala	Val	Glu	Leu	Gly	Leu	His	Leu	His	Ile	Gly	Gln	Gly	Asp
				85					90					95	
Thr	Pro	Tyr	Thr	Gln	Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu
			100					105					110		
Gly	Leu	Ser	Ile	Glu	Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln
		115					120					125			
Cys	Ala	Glu	Thr	Gly	Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro
	130					135					140				
Val	Ala	Ser	Thr	Ala	Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val
145					150					155					160
Glu	Gly	Ile	Ala	Glu	Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala
				165				170						175	
Ser	Val	Ala	Ile	Gly	Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala
			180					185					190		
Ala	Thr	Pro	Ile	Asp	Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala
		195					200					205			
Ala	Asn	Pro	Ala	Ala	Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro
	210					215					220				
Thr	Phe	Ser	Pro	Glu	Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln
225					230					235					240
Gly	Ala	Phe	Val	Asn	Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala
				245					250					255	
Gly	Thr	Asp	Pro	Thr	Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser
			260					265					270		
Ile	Ala	Ala	Gly	Gly	Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val
			275				280					285			

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
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<210> 541
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1528)
 <223> FRXA01209

<400> 541
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 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528

Ala Ala Gly Glu Ser Val Glu
470 475

<210> 542

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 542

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20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

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<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01413

<400> 543

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 cgggtttcct cagcgttttaa ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115
 Leu Thr His Leu Phe
 1 5

 tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
 10 15 20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
 Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
 25 30 35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
 40 45 50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
 Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
 55 60 65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
 Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
 70 75 80 85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
 Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
 90 95 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
 Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
 105 110 115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
 Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
 120 125 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
 Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
 135 140 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
 Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
 150 155 160 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
 Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
 170 175 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
 Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
 185 190 195

gac aac aag tagagtttta aaataccgat caa 723
 Asp Asn Lys
 200

<210> 544

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
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Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
 20 25 30



Gln	His	Leu	Arg	Asn	Ser	Pro	Asn	Asp	Leu	Gln	Gly	Leu	Lys	Ile	Arg
		35				40						45			
Trp	Cys	Glu	Leu	Tyr	Ser	Thr	Thr	Gly	Lys	Asp	Gln	Gly	Val	Glu	Leu
		50				55				60					
Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	Phe	Glu	Ala	Ser	Thr
				70						75				80	
Leu	Ser	Gly	Leu	Glu	Lys	Leu	Glu	Thr	Val	Glu	Asp	Leu	Lys	Glu	Ala
				85				90						95	
Ala	Arg	Leu	Ile	Tyr	Glu	Gln	Gly	Pro	Gln	Tyr	Val	Val	Val	Lys	Gly
		100						105				110			
Gly	Met	Asp	Phe	Pro	Gly	Glu	Asn	Ala	Val	Asp	Val	Leu	Phe	Asp	Gly
		115				120						125			
Ser	Ser	Tyr	His	Val	Phe	Ser	Glu	Pro	Lys	Ile	Gly	Glu	Glu	Arg	Val
		130				135				140					
Ser	Gly	Ala	Val	Cys	Thr	Phe	Ala	Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala
145				150						155				160	
Lys	Gly	Ala	Glu	Val	Val	Asp	Pro	Val	Ala	Thr	Ala	Lys	Arg	Val	Val
				165				170						175	
Thr	Arg	Ala	Val	Gln	Asp	Ala	Val	Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser
		180						185				190			
Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys								
		195				200									

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(772)
<223> RXN01617
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tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
Leu Ile Leu Lys Thr
1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
25 30 35

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

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40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		

cct 795

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<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 546

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
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Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 547

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 547

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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
	85	90	95
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
	100	105	110
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
	115	120	125
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
	130	135	140
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
	145	150	155
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
	165	170	175
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
	180	185	190
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
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aaacaagctc cct			638

<210> 548

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val			
1	5	10	15
Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr			
	20	25	30
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu			
	35	40	45
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			

50 55 60
 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

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 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(892)
 <223> RXS01807

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 Met Pro Ser Ala Gly
 1 5
 gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
 10 15 20
 gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
 25 30 35
 ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
 40 45 50
 gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
	250	255	260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
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 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
 20 25 30
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 551

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXC01021



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<210> 552
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
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Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1             5             10             15
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Ser	Val	Gln	Pro	Glu	Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala		
			20						25				30				
Ala	Ser	Lys	Glu	Ala	Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu		
		35					40					45					
Trp	Ala	Arg	Thr	Ala	Val	Glu	Gln	Leu	Ser	Glu	Arg	Arg	Ala	Glu	Ile		
	50					55					60						
Asn	Ala	Leu	Asn	Val	Phe	Pro	Val	Pro	Asp	Ala	Asp	Thr	Gly	Ser	Asn		
	65				70					75					80		
Met	Thr	Tyr	Thr	Met	Thr	Ala	Ala	Leu	Asp	Glu	Ala	Leu	Lys	Leu	Gly		
				85					90					95			
Glu	Leu	Gly	Asp	Val	Ala	Arg	Ile	Thr	Glu	Ala	Leu	Ala	Val	Gly	Ser		
			100					105					110				
Val	Arg	Gly	Ala	Arg	Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu		
		115					120					125					
Arg	Ala	Ile	Ala	Gln	Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr		
	130					135					140						
Ile	Gln	Glu	Ala	Leu	Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile		
	145				150					155					160		
Thr	Asp	Pro	Val	Glu	Gly	Thr	Val	Val	Thr	Val	Leu	Arg	Ser				
				165					170								

<210> 553
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1084)
 <223> RXN02246

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 caacaaggcg atccaggagt tgcgagcact cgcgagctaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50

gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
	55					60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggc	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
	70				75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
				90					95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggc	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggc	ttt	gct	ggc	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
	150				155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170				175					180			
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggc	acc	ggc	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185				190						195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggc	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
	230				235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggc	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
			250					255					260			
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265				270						275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
		280				285						290				



aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
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Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 555
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> FRXA02246

<400> 555
 tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60
 caacaaggcg atccaggagt tgcgagcact cgcgagtaaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga

1107

Lys Glu His

<210> 556

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
1 5 10 15Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20 25 30Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
210 215 220Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
225 230 235 240Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
245 250 255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 557

<211> 756

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(733)

<223> RXA02247

<400> 557

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ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115
 Met Phe Thr Gly Ile
 1 5

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser
 10 15 20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu
 25 30 35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe
 40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg
 55 60 65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg
 70 75 80 85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His
 90 95 100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp
 105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
200 205 210

taggttagac aacgtgagtg aac 756

<210> 558

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu
1 5 10 15

His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
 195 200 205
 Thr Arg Asp
 210

<210> 559
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXN02248

<400> 559
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 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa
 1389

Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
 1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp
 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 561

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> FRXA02248

<400> 561

gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85

cag gat gcc cgc gcc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100

ggc acc aca gcc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210
 ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225
 ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245
 gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260
 gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275
 cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290
 gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305
 ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325
 ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340
 gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355
 cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370
 gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385
 gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405
 gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu

410

415

420

aac taaggagcac aacaatggct aaa

1389

Asn

<210> 562

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

Val	Ser	Glu	His	Glu	Gln	Ala	His	Ser	Gln	Leu	Asp	Ser	Val	Glu	Glu
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Ala	Ile	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Ala	Val	Val	Val	Val	Asp	Asp
			20					25						30	

Glu	Asp	Arg	Glu	Asn	Glu	Gly	Asp	Ile	Ile	Phe	Ala	Ala	Glu	Leu	Ala
	35						40					45			

Thr	Pro	Glu	Leu	Val	Ala	Phe	Met	Val	Arg	Tyr	Ser	Ser	Gly	Tyr	Ile
	50					55					60				

Cys	Ala	Pro	Leu	Thr	Ala	Lys	Asp	Ala	Asp	Arg	Leu	Asp	Leu	Pro	Pro
65					70					75					80

Met	Thr	Ala	His	Asn	Gln	Asp	Ala	Arg	Gly	Thr	Ala	Tyr	Thr	Val	Thr
				85					90					95	

Val	Asp	Ala	Asn	Thr	Gly	Thr	Thr	Gly	Ile	Ser	Ala	Thr	Asp	Arg	Ala
			100					105						110	

His	Thr	Leu	Arg	Leu	Leu	Ala	Asp	Pro	Glu	Ala	Asp	Arg	Thr	Asp	Phe
		115					120					125			

Thr	Arg	Pro	Gly	His	Val	Val	Pro	Leu	Arg	Ala	Arg	Glu	Gly	Gly	Val
	130					135					140				

Leu	Val	Arg	Ala	Gly	His	Thr	Glu	Ala	Ala	Val	Asp	Leu	Ala	Arg	Ala
145					150					155					160

Ala	Gly	Leu	Arg	Pro	Ala	Gly	Val	Ile	Cys	Glu	Val	Val	Ser	Glu	Glu
				165					170					175	

Asp	Pro	Thr	Gly	Met	Ala	Arg	Val	Pro	Glu	Leu	Arg	Arg	Phe	Cys	Asp
			180					185					190		

Glu	His	Asp	Leu	Lys	Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg
		195					200					205			

Arg	Lys	Asn	Glu	Ile	Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro
	210					215					220				

Thr	Asp	Phe	Gly	Thr	Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp
225					230					235					240

Gly	Thr	Glu	Leu	Val	Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly
			245						250					255	

Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

 <210> 563
 <211> 600
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(577)
 <223> RXN02249

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 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
150 155

ttg 600

<210> 564

<211> 159

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 150 155

ttg 600

<210> 566
 <211> 159
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 566
 Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 567
 <211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXA02250

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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
 Val Thr Thr Asn Ala

	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val			
	10	15	20
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr			
	25	30	35
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Lys Pro Trp Glu Leu Glu Val			
	40	45	50
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile			
	55	60	65
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr			
	70	75	80
ggg gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly			
	90	95	100
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val			
	105	110	115
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg			
	120	125	130
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser			
	135	140	145
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp			
	150	155	160
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr			
	170	175	180
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp			
	185	190	
gtggctgac caa			702

<210> 568

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Val Thr Thr Asn Ala Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala
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His Ser Gly Ala Val Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu
 20 25 30
 Ile Gln Glu Tyr Thr Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro
 35 40 45
 Trp Glu Leu Glu Val Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val
 50 55 60
 Ala Val Val Val Ile Met Ala Val His Ile Phe Met Gly Ala Val Val
 65 70 75 80
 Asp Val Asp Phe Thr Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala
 85 90 95
 Phe Pro Ala Leu Gly Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu
 100 105 110
 Thr Arg Pro Arg Val Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn
 115 120 125
 Phe Ile Gly Thr Arg Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser
 130 135 140
 Phe Pro Lys Gly Ser Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu
 145 150 155 160
 Phe Val Pro Met Trp Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val
 165 170 175
 Arg Ala Val Ala Thr Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu
 180 185 190
 Asp

<210> 569
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXA01489

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 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
 Val Asp Ile Trp Ser
 1 5
 gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
 Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
 10 15 20
 ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
 Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

25										30					35					
gcc	aag	aag	cag	gcc	gag	gag	ctg	ggg	gtg	cct	tgt	gtc	atg	gtg	acc	259				
Ala	Lys	Lys	Gln	Ala	Glu	Glu	Leu	Gly	Val	Pro	Cys	Val	Met	Val	Thr					
		40					45					50								
ttt	gac	ccg	cat	ccg	atc	gct	gtg	ttt	ttg	cca	ggg	aaa	gag	cca	acc	307				
Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro	Gly	Lys	Glu	Pro	Thr					
	55					60					65									
cgt	ttg	gct	cct	ttg	gat	tat	cgc	ctt	aat	ttg	gct	gcg	gaa	tgt	ggc	355				
Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	Ala	Ala	Glu	Cys	Gly					
	70				75					80					85					
gtc	gat	gct	gcg	ttg	gtt	att	gat	ttc	act	aaa	gaa	ctc	gca	ggg	ctg	403				
Val	Asp	Ala	Ala	Leu	Val	Ile	Asp	Phe	Thr	Lys	Glu	Leu	Ala	Gly	Leu					
				90					95					100						
agc	gct	gaa	gag	tat	ttc	aca	acc	atg	atc	gtg	gat	acg	ctg	cat	gcg	451				
Ser	Ala	Glu	Glu	Tyr	Phe	Thr	Thr	Met	Ile	Val	Asp	Thr	Leu	His	Ala					
			105					110					115							
cgt	tca	gtt	gtg	gtg	ggg	gag	aac	ttc	acc	ttc	ggg	gtc	aat	ggc	gct	499				
Arg	Ser	Val	Val	Val	Gly	Glu	Asn	Phe	Thr	Phe	Gly	Val	Asn	Gly	Ala					
		120					125					130								
ggc	act	gag	tcc	acg	atg	cgg	gaa	ttg	gga	caa	aag	ttt	ggc	gtg	aat	547				
Gly	Thr	Glu	Ser	Thr	Met	Arg	Glu	Leu	Gly	Gln	Lys	Phe	Gly	Val	Asn					
	135					140					145									
gtc	acg	att	gct	ccg	ctg	ctg	cat	gat	gat	gac	cag	cgt	att	tgc	tcc	595				
Val	Thr	Ile	Ala	Pro	Leu	Leu	His	Asp	Asp	Asp	Gln	Arg	Ile	Cys	Ser					
	150				155					160					165					
acc	ttg	gtg	cgc	gat	tac	ttg	gat	cag	ggc	gag	gtt	gag	cgc	gcg	aac	643				
Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn					
				170				175						180						
tgg	gcg	ctt	ggg	cga	cgc	tat	gcc	gtg	cgc	ggc	gaa	gtt	gtc	cgt	ggg	691				
Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly	Glu	Val	Val	Arg	Gly					
		185					190					195								
gct	ggc	cgt	ggc	ggc	aaa	gaa	ttg	ggc	tat	ccc	acc	gcg	aat	ctc	tac	739				
Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro	Thr	Ala	Asn	Leu	Tyr					
		200					205					210								
ctg	ccg	acc	tct	gtg	gcg	ctg	ccc	gcc	gat	ggc	gtg	tat	gca	ggc	tgg	787				
Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly	Val	Tyr	Ala	Gly	Trp					
		215				220					225									
ttc	acc	atc	acc	gat	gac	cgc	gaa	atc	gac	aag	gaa	atc	tcc	cgc	gat	835				
Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys	Glu	Ile	Ser	Arg	Asp					
	230				235					240					245					
atc	gac	ggc	acc	atg	gtt	cca	ggc	gtg	cgt	tac	caa	act	gcc	att	tcc	883				
Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr	Gln	Thr	Ala	Ile	Ser					
				250				255						260						
gtg	ggc	acc	aat	ccc	acc	ttc	ggc	gat	gag	cga	cgc	agc	gtc	gag	gca	931				
Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg	Arg	Ser	Val	Glu	Ala					
			265					270					275							



ttc	atc	ctc	gac	cag	gaa	gcc	gac	ctg	tac	ggg	cac	cat	gtc	atg	gtg	979
Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly	His	His	Val	Met	Val	
		280					285					290				

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
1027
Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
1075
Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
1123
Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
330 335 340

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1146

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<210> 570
<211> 341
<212> PRT
<213> Corynebacterium glutamicum
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20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
 340

 <210> 571
 <211> 1197
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
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 <222> (101)..(1174)
 <223> RXA02135

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 aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
 Met Val Pro Ala Glu
 1 5

 ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
 10 15 20

 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
 25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979



Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290
 gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg
 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
 295 300 305
 tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag
 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325
 att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc
 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340
 gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg
 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
 345 350 355
 gag taacttttcta agcgatgtcc ggc
 1197
 Glu

<210> 572
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 572
 Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys
 1 5 10 15
 Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
 340 345 350
 Pro Glu Gln Asn Thr Glu
 355

<210> 573
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXA01489

<400> 573
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 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
 Val Asp Ile Trp Ser
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883



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<210> 574
<211> 341
<212> PRT
<213> Corynebacterium glutamicum
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130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
 340

<210> 575

<211> 805

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (87)..(782)

<223> RXN01712

<400> 575

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taaacaagct ggcctagact tgaaacatg gtc gat atc ttg gaa ctc atc ggt 113
 Met Val Asp Ile Leu Glu Leu Ile Gly
 1 5

ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile	110	115	120	
acg gat aat tcc gat caa gca aag cag cag ccg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys	220	225	230	
tgagtgttgg actctccgga tct				805

<210> 576

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

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Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr
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Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr
          20           25           30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
      35           40           45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
 50           55           60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
 65           70           75           80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
          85           90           95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
          100          105          110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
      115           120          125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
      130           135          140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
      145           150          155          160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
          165          170          175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
          180          185          190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
      195           200          205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
      210           215          220

Phe Leu Arg Tyr Lys Arg Ala Lys
      225           230

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<210> 577

<211> 578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (55)..(555)

<223> FRXA01712

<400> 577

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cttctgttgg cgcttcgcag gtgggtcggac gtggtgttgg ttgggtcgag cacggtg
                               57
                               Val

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1

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aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
      5                      10                      15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20                      25                      30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
      35                      40                      45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
      50                      55                      60                      65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
      70                      75                      80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
      85                      90                      95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
      100                      105                      110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
      115                      120                      125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
      130                      135                      140                      145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
      150                      155                      160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578
Arg Tyr Lys Arg Ala Lys
      165

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<210> 578

<211> 167

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 578

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Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
  1                      5                      10                      15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
      20                      25                      30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
      35                      40                      45

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Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
 50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
 65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
 85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
 100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
 115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
 130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
 145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys
 165

<210> 579

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXN02384

<400> 579

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aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
 Val Thr Arg Arg Leu
 1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
 10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
 25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
 40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
 55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		

<210> 580

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn	
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Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu	
20 25 30	

Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn	
35 40 45	

Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala	
50 55 60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
65 70 75 80

Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
85 90 95

Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
100 105 110

Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
115 120 125

Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
130 135 140

Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
145 150 155 160

Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
165 170 175

Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
180 185 190

Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
195 200 205

Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
210 215 220

Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
225 230 235

<210> 581

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN01560

<400> 581

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tgcacagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
Val Gly Val Ser Tyr
1 5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
10 15 20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
25 30 35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
	90	95	100
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
	105	110	
ttt			453

<210> 582
 <211> 110
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 582
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 Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30
 Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95
 Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 583
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXN00667

<400> 583
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Met Ile Ala Leu Lys
1 5

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta 163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
10 15 20

ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac 211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
25 30 35

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg 259
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
40 45 50

cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt 307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
55 60 65

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc 355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
70 75 80 85

gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc 403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
90 95 100

gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac 451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
105 110 115

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct 499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
120 125 130

cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg 547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
135 140 145

act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act 595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
150 155 160 165

tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac 643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
170 175 180

caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag gca atc 691
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu Ala Ile
185 190 195

gca gaa ttc gtt cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa 739
Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Glu
200 205 210

tcc cgc atc gaa aaa gaa cgc ggc atc gtg caa gcc ttc gtc gtg gaa 787
Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln Ala Phe Val Val Glu
215 220 225

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ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg
 1027
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag
 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt
 1124
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu
 330 335

agacatcacc cag
 1137

<210> 584

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 584

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Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
 130 135 140
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
 145 150 155 160
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
 165 170 175
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
 180 185 190
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly
 195 200 205
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln
 210 215 220
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser
 225 230 235 240
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His
 245 250 255
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly
 260 265 270
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile
 275 280 285
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp
 290 295 300
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp
 305 310 315 320
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly
 325 330 335
 Ser Leu

<210> 585
 <211> 1281
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(1258)
 <223> RXC01711

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 gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg ggc 115

											Met	Leu	Leu	Met	Ala	
											1					5
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc	163
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe	
				10					15					20		
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggc	att	ccg	gtc	211
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val	
			25					30					35			
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg	259
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro	
		40					45					50				
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg	307
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr	
	55					60					65					
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta	355
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu	
70					75					80					85	
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggc	tgg	gcg	ctg	cgc	agc	atg	403
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met	
				90					95					100		
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa	451
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln	
			105					110					115			
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg	499
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu	
		120					125					130				
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga	547
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly	
	135					140					145					
cta	gtc	att	ggc	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt	595
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu	
150					155					160					165	
ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tgc	ctc	atc	ctc	ggc	643
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly	
			170						175					180		
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg	691
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro	
			185					190					195			
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggc	gaa	act	739
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr	
		200					205					210				
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga	787
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly	
	215					220					225					
atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg	835
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met	

230	235	240	245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca				883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro				
250		255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc				931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe				
265		270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct				979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro				
280		285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt				
1027				
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val				
295		300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc				
1075				
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser				
310		315	320	325
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc				
1123				
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr				
330		335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc				
1171				
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile				
345		350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att				
1219				
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile				
360		365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt				
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Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala				
375		380	385	
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1281				

<210> 586

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

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Val	Thr	Asp	Asp	Phe	Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val
		20						25					30		

Glu	Gly	Ile	Pro	Val	Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



35					40					45					
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr
50						55					60				
Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu
65					70					75					80
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp
				85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu
			100					105					110		
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile
		115					120					125			
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys
130						135					140				
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro
145					150					155					160
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly
				165					170					175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala
			180					185					190		
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro
		195					200					205			
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu
	210					215					220				
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu
225					230					235					240
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe
				245					250					255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu
			260					265					270		
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser
		275					280					285			
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val
	290					295					300				
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro
305					310					315					320
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu
				325					330					335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe
			340					345					350		
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr
		355					360					365			

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
 370 375 380

Thr Ala
 385

<210> 587
 <211> 777
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(754)
 <223> RXC02380

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 tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115
 Met Thr Thr Thr Val
 1 5
 aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20
 cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35
 ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50
 aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65
 gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85
 cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100
 caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115
 gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130
 cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145



att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
 200 205 210

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 Gly Gln Asn Gln Ala
 215

<210> 588

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly
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 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

180	185	190	
Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys			
195	200	205	
Asp Met Asp Pro Lys Gly Gln Asn Gln Ala			
210	215		
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	Met Thr Thr Thr Val		
	1 5		
aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att		163	
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile			
10 15 20			
cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat		211	
His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp			
25 30 35			
ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg		259	
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala			
40 45 50			
aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc		307	
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile			
55 60 65			
gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat		355	
Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp			
70 75 80 85			
cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag		403	
Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys			
90 95 100			
caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg		451	
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu			
105 110 115			
gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc		499	
Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala			
120 125 130			
cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc		547	
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile			
135 140 145			

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
 200 205 210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777
 Gly Gln Asn Gln Ala
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<210> 590

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 590

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly
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Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val
 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
 180 185 190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala
 210 215

<210> 591
 <211> 594
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(571)
 <223> RXC02921

<400> 591
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aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa 115
 Val Ser Ala Leu Glu
 1 5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163
 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
 10 15 20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
 25 30 35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
 40 45 50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307
 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
 55 60 65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac 355
 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
 70 75 80 85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403
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 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
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 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
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 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
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Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
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Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
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Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
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 745 750 755

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 2419
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
 760 765 770

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 2467
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
 775 780 785

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 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
 825 830 835



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 Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
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 855 860 865

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 890 895 900

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 920 925 930

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 2947
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Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
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 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
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 930 935 940
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 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
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 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
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 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp
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 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln
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 aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
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 135 140 145
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 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
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ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
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 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
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 20 25 30

 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45

 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60

 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80

 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95

 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110

 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125

 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140

 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
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<210> 597
 <211> 1461
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1438)
 <223> RXN02754

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 agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
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 gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35
 ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50
 tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65
 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85
 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

	90	95	100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act				451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr				
	105	110	115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg				499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu				
	120	125	130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg				547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met				
	135	140	145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc				595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg				
	150	155	160	165
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct				643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala				
	170	175	180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att				691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile				
	185	190	195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac				739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn				
	200	205	210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa				787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu				
	215	220	225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc				835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr				
	230	235	240	245
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc				883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly				
	250	255	260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc				931
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg				
	265	270	275	
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc				979
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser				
	280	285	290	
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt				
1027				
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val				
	295	300	305	
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca				
1075				
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro				
	310	315	320	325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
 1458
 Arg Phe Val Gly Phe Pro Pro Ala Ala
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aac
 1461

<210> 598

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
 20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60



Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
 385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
 405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
 420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
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<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(871)

<223> FRXA02405

<400> 599

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agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
 90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
 Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
 105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
 Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
 120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
 Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
 135 140 145

gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
 Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
 150 155 160 165

acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
 Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
 170 175 180

gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691
 Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
 185 190 195

cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
 Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
 200 205 210

gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
 Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
 215 220 225

tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
 Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
 230 235 240 245

caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871
 Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro
 250 255

<210> 600

<211> 257

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 600

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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
 20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255

Pro

<210> 601
 <211> 509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(486)
 <223> FRXA02754

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atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80


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ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                      105                      110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                      120                      125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                      135                      140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
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gcc gct tagacaattc ggtctcacca aac 509
Ala Ala

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<210> 602

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 602

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Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
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Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
      20              25              30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
      35              40              45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
      50              55              60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
      65              70              75              80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85              90              95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100              105              110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115              120              125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130              135              140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
      145              150              155              160

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Ala Ala

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<210> 603
<211> 960
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(937)  
<223> RXA02112
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agctcctggtt actcctagct cctcgaagga tgcgtaattt				atg Met	act Thr	acc Thr	cat His	att Ile	115							
					1											5
gac	cgc	atc	gtt	ggc	gca	gcg	tta	tcc	gag	gat	gcg	cca	tgg	ggc	gac	163
Asp	Arg	Ile	Val	Gly	Ala	Ala	Leu	Ser	Glu	Asp	Ala	Pro	Trp	Gly	Asp	20
				10					15							
att	acc	tcc	gac	act	ttt	atc	cca	gga	tcg	gcg	cag	ctg	agc	gcc	aag	211
Ile	Thr	Ser	Asp	Thr	Phe	Ile	Pro	Gly	Ser	Ala	Gln	Leu	Ser	Ala	Lys	35
			25					30								
gtt	gtt	gcc	cgg	gag	cca	ggg	gtg	ttc	agc	ggg	cag	gcg	ctt	tta	gac	259
Val	Val	Ala	Arg	Glu	Pro	Gly	Val	Phe	Ser	Gly	Gln	Ala	Leu	Leu	Asp	50
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gcc	tcc	ttc	cgg	ctc	gtc	gat	cct	agg	ata	aac	gca	tcc	ctt	aag	gtg	307
Ala	Ser	Phe	Arg	Leu	Val	Asp	Pro	Arg	Ile	Asn	Ala	Ser	Leu	Lys	Val	65
	55					60										
gct	gat	ggg	gac	agc	ttt	gaa	acc	ggg	gac	atc	cta	gga	aca	att	acc	355
Ala	Asp	Gly	Asp	Ser	Phe	Glu	Thr	Gly	Asp	Ile	Leu	Gly	Thr	Ile	Thr	85
	70				75					80						
ggc	agt	gct	aga	agc	atc	ctc	cgt	tca	gag	cgc	att	gct	ctc	aac	ttc	403
Gly	Ser	Ala	Arg	Ser	Ile	Leu	Arg	Ser	Glu	Arg	Ile	Ala	Leu	Asn	Phe	100
				90					95							
att	cag	agg	acg	tcc	ggc	atc	gct	aca	ttg	aca	tcg	tgc	tat	gtt	gca	451
Ile	Gln	Arg	Thr	Ser	Gly	Ile	Ala	Thr	Leu	Thr	Ser	Cys	Tyr	Val	Ala	115
			105				110									
gag	gtt	aaa	ggc	acc	aaa	gcc	cgc	att	gtt	gat	acc	cgg	aaa	acc	aca	499
Glu	Val	Lys	Gly	Thr	Lys	Ala	Arg	Ile	Val	Asp	Thr	Arg	Lys	Thr	Thr	130
		120					125									
ccc	ggc	ctg	cgc	atc	att	gaa	cgc	caa	gct	gtc	cgt	gac	ggg	ggc	gga	547
Pro	Gly	Leu	Arg	Ile	Ile	Glu	Arg	Gln	Ala	Val	Arg	Asp	Gly	Gly	Gly	145
		135				140										
ttt	aat	cac	cga	gcc	acc	ttg	tcc	gat	gct	gtc	atg	gtg	aaa	gat	aac	595
Phe	Asn	His	Arg	Ala	Thr	Leu	Ser	Asp	Ala	Val	Met	Val	Lys	Asp	Asn	165
150					155					160						

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
 170 175 180
 tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
 185 190 195
 gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
 200 205 210
 acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
 215 220 225
 gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
 230 235 240 245
 ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
 250 255 260
 gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
 265 270 275
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 Ile Phe

<210> 604

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

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 20 25 30
 Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
 35 40 45
 Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60
 Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
 65 70 75 80
 Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
 85 90 95
 Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
 115 120 125
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
 130 135 140
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
 145 150 155 160
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
 165 170 175
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
 180 185 190
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
 210 215 220
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala
 225 230 235 240
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
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 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
 260 265 270
 Asp Leu Gly Leu Asp Ile Phe
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<210> 605
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1384)
 <223> RXA02111

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 Met Thr Thr Ser Ile
 1 5
 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20
 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
 25 30 35
 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40										45					50					
ccg	cgc	cag	cag	gtt	ctc	ccc	gag	gag	tac	cag	cgc	gca	agt	gat	gac	307				
Pro	Arg	Gln	Gln	Val	Leu	Pro	Glu	Glu	Tyr	Gln	Arg	Ala	Ser	Asp	Asp					
55				60				65												
gaa	ctg	cat	cgt	agg	atc	cgg	gaa	gcg	aaa	gac	acc	ctg	ggg	gac	aaa	355				
Glu	Leu	His	Arg	Arg	Ile	Arg	Glu	Ala	Lys	Asp	Thr	Leu	Gly	Asp	Lys					
70				75				80				85								
gtg	gtt	atc	cta	gga	cac	ttc	tac	cag	cgc	gat	gaa	gtt	atc	caa	cac	403				
Val	Val	Ile	Leu	Gly	His	Phe	Tyr	Gln	Arg	Asp	Glu	Val	Ile	Gln	His					
90				95				100												
gca	gat	ttt	gtt	ggg	gac	tct	ttc	caa	ctt	gcc	cgc	gct	gcc	aaa	acc	451				
Ala	Asp	Phe	Val	Gly	Asp	Ser	Phe	Gln	Leu	Ala	Arg	Ala	Ala	Lys	Thr					
105				110				115												
cga	ccc	gag	gcg	gaa	gag	att	gtg	ttc	tgc	ggg	gtg	cac	ttc	atg	gct	499				
Arg	Pro	Glu	Ala	Glu	Ala	Ile	Val	Phe	Cys	Gly	Val	His	Phe	Met	Ala					
120				125				130												
gaa	acc	gct	gat	ctg	tta	tcc	acg	gat	gaa	caa	tca	gtg	atc	ctc	ccc	547				
Glu	Thr	Ala	Asp	Leu	Leu	Ser	Thr	Asp	Glu	Gln	Ser	Val	Ile	Leu	Pro					
135				140				145												
aac	ctt	gcc	gca	ggg	tgc	tcc	atg	gca	gac	atg	gct	gac	ctt	gat	tcc	595				
Asn	Leu	Ala	Ala	Gly	Cys	Ser	Met	Ala	Asp	Met	Ala	Asp	Leu	Asp	Ser					
150				155				160				165								
gtc	gaa	gac	tgc	tgg	gag	caa	ctc	acc	tca	att	tat	ggc	gat	gac	acc	643				
Val	Glu	Asp	Cys	Trp	Glu	Gln	Leu	Thr	Ser	Ile	Tyr	Gly	Asp	Asp	Thr					
170				175				180												
ctg	atc	cct	gtg	acc	tac	atg	aat	tcc	tct	gca	gag	ctc	aaa	ggg	ttc	691				
Leu	Ile	Pro	Val	Thr	Tyr	Met	Asn	Ser	Ser	Ala	Ala	Leu	Lys	Gly	Phe					
185				190				195												
gtg	ggg	gag	cac	ggc	gga	att	gta	tgc	acc	tcc	tca	aat	gca	cgt	tcc	739				
Val	Gly	Glu	His	Gly	Gly	Ile	Val	Cys	Thr	Ser	Ser	Asn	Ala	Arg	Ser					
200				205				210												
gta	ttg	gag	tgg	gag	ttt	gaa	cgc	ggc	caa	cga	gtc	ctg	ttc	ttc	ccc	787				
Val	Leu	Glu	Trp	Ala	Phe	Glu	Arg	Gly	Gln	Arg	Val	Leu	Phe	Phe	Pro					
215				220				225												
gat	cag	cac	ttg	ggg	cga	aac	acc	gag	aaa	gcc	atg	ggc	att	ggg	atc	835				
Asp	Gln	His	Leu	Gly	Arg	Asn	Thr	Ala	Lys	Ala	Met	Gly	Ile	Gly	Ile					
230				235				240				245								
gat	caa	atg	ccc	ctg	tgg	aat	ccc	aac	aaa	cca	ctg	ggg	ggc	aac	acc	883				
Asp	Gln	Met	Pro	Leu	Trp	Asn	Pro	Asn	Lys	Pro	Leu	Gly	Gly	Asn	Thr					
250				255				260												
gtt	tcc	gag	cta	gaa	aac	gca	aag	gta	ctg	ctc	tgg	cat	ggg	ttc	tgc	931				
Val	Ser	Glu	Leu	Glu	Asn	Ala	Lys	Val	Leu	Leu	Trp	His	Gly	Phe	Cys					
265				270				275												
tct	gta	cac	aag	cgc	ttt	act	gtc	gag	cag	atc	aac	aaa	gcc	cgc	gcc	979				
Ser	Val	His	Lys	Arg	Phe	Thr	Val	Glu	Gln	Ile	Asn	Lys	Ala	Arg	Ala					
280				285				290												

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act
1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
410 415 420

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1407

Pro Ser Ser Ser Lys Asp Ala
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<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

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Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45



Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
 370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
 385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
 405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
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<210> 607
 <211> 954
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(931)
 <223> RXA01073

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 Met Thr Asn Thr Gln
 1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163
 Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
 10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211
 Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala
 25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259
 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
 40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307
 Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala
 55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355
 Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr
 70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403
 Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile
 90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451
 Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala
 105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499
 Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp
 120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr
 135 140 145

 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala
 150 155 160 165

 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala
 170 175 180

 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr
 200 205 210

 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu
 215 220 225

 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp
 230 235 240 245

 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg
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 taatccaaca gtttgagtgt cgc 954

<210> 608

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 608

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 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
 35 40 45

 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
 50 55 60

 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
 65 70 75 80

Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val
 85 90 95
 Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys
 100 105 110
 Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu
 115 120 125
 Pro Glu Leu Thr Asp Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg
 130 135 140
 Met Val Ala Gln Tyr Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile
 145 150 155 160
 Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe
 165 170 175
 Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg
 180 185 190
 Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp
 195 200 205
 Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro
 210 215 220
 Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu
 225 230 235 240
 Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His
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 Leu Trp Lys Val Gly Gln His Lys Arg His Leu Pro Ala Thr Pro Gln
 260 265 270
 Glu Asn Trp Trp Arg
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<210> 609

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXN02754

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 Val Asn Thr Asn Pro
 1 5
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc	211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg	
25 30 35	
ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
40 45 50	
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac	307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
55 60 65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac	355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg
 265 270 275
 aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
 280 285 290
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt
 1027
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305
 gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca
 1075
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355
 gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370
 cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405
 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
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 Arg Phe Val Gly Phe Pro Pro Ala Ala
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 aac
 1461

<210> 610
 <211> 446
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 610

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Gly	Ser	Ala	Glu	Arg	Pro	Ser	Thr	Phe	Glu	Val	Phe	Ser	Arg	Arg	Leu
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Pro	Asn	Glu	Arg	Arg	Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu
	50					55					60				
Lys	Ala	Ile	Arg	Asp	Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu
65					70					75					80
Asp	Phe	Leu	Asp	Asp	Arg	Thr	Leu	Glu	Tyr	Leu	Arg	Asn	Tyr	Arg	Phe
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Ser	Pro	Leu	Leu	Thr	Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu
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Glu	Thr	Val	Ile	Leu	Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser
	130					135					140				
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Met	Gly	Ser	Arg	Arg	Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg
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Ala	Ala	Tyr	Leu	Ala	Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala
			180					185					190		
Tyr	Arg	Tyr	Gly	Ile	Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr
		195					200					205			
Leu	Leu	His	Ile	Asn	Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe
	210					215					220				
Lys	Ala	Gln	Val	Glu	Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp
225					230					235					240
Thr	Tyr	Asp	Ile	Thr	Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly
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Pro	Asp	Leu	Gly	Gly	Val	Arg	Ile	Asp	Ser	Gly	Asp	Leu	Gly	Val	Leu
		260						265					270		
Ala	Arg	Lys	Val	Arg	Lys	Gln	Leu	Asp	Asp	Leu	Asn	Ala	His	Asn	Thr
		275					280					285			
Lys	Ile	Val	Val	Ser	Ser	Asp	Leu	Asp	Glu	Phe	Ala	Ile	Ala	Gly	Leu

290	295	300
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Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val 325 330 335		
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly 340 345 350		
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile 355 360 365		
Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys 370 375 380		
Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile 385 390 395 400		
Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys 405 410 415		
Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu 420 425 430		
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<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02299

<400> 611

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                                         1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
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tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
                        25 30 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
                        40 45 50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile

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55	60	65	
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg			355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
70	75	80	85
atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
90	95		100
gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc			451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
105	110		115
ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg			499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
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aga agc att tagcgtttta gctcgccaat att			531
Arg Ser Ile			
135			

<210> 612

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
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Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
20 25 30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
35 40 45

Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
50 55 60

Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
65 70 75 80

Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
85 90 95

Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
100 105 110

Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
115 120 125

Gly Leu Leu Thr Ser Arg Ser Ile
130 135

<210> 613

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

<400> 613

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tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
                                         Met Gln Val Ala Thr
                                         1                               5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
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ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
                        25                        30                        35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
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aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
                        55                        60                        65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
                        70                        75                        80                        85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
                        90                        95                        100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
                        105                        110                        115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
                        120                        125                        130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
                        135                        140                        145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
                        150                        155                        160                        165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
                        170                        175                        180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
                        185                        190                        195

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caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
 200 205 210
 gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
 215 220 225
 agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
 230 235 240 245
 acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
 250 255 260
 gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275
 gag ctc tagtaccaac cctgcgttgc agc 960
 Glu Leu

<210> 614
 <211> 279
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 614
 Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
 1 5 10 15
 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30
 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45
 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60
 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80
 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95
 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110
 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125
 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140
 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
 260 265 270

Leu Ile Asp Asn Ile Glu Leu
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<210> 615

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXN01929

<400> 615

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ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
 Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 616

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
 130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

<210> 617

<211> 930

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 617

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				Met	Ser	Gly	Ile	Asp	
				1				5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163								
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly									
	10								
	15								
	20								
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211								
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile									
	25								
	30								
	35								
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259								
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala									
	40								
	45								
	50								
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307								
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu									
	55								
	60								
	65								
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355								
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu									
	70								
	75								
	80								
	85								
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403								
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln									
	90								
	95								
	100								
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451								
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala									
	105								
	110								
	115								
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499								
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile									
	120								
	125								
	130								
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547								
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln									
	135								
	140								
	145								
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595								
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser									
	150								
	155								
	160								
	165								
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643								
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala									
	170								
	175								
	180								
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691								
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val									
	185								
	190								
	195								
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739								
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly									
	200								
	205								
	210								
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787								
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg									
	215								
	220								
	225								

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

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cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
 Leu Ser Phe Thr His
 1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
 10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
 25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
 40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
 55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
 70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
 90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
 105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
 120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
	230	235	240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
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aaa aac atc gaa ggc tgatcccggt ttacccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		

<210> 620

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
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Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
20 25 30

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
35 40 45

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Ala Tyr Ala
50 55 60

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
65 70 75 80

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
85 90 95

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
100 105 110



Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
 115 120 125
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
 130 135 140
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
 145 150 155 160
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
 165 170 175
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala
 180 185 190
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln
 195 200 205
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly
 210 215 220
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala
 225 230 235 240
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro
 245 250 255
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly
 260 265

<210> 621

<211> 1137

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 621

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 cttttcacca aaatttttac gaaaggcgag atttttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 622

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 622

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190



Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

<210> 623
 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> FRXA01145

<400> 623
 taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145
 tgc ctc atc 556
 Cys Leu Ile
 150

<210> 624

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15
 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101) .. (1366)
<223> RXA02239

<400> 625
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gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115
Val Pro Met Thr His
1 5
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly
10 15 20
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu
25 30 35
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe
40 45 50
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr
55 60 65
acg gtg ttt gat gcg gtg gat tcc gtg cag cat gtg aaa gtt ggc cag 355
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln
70 75 80 85
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala
90 95 100
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu
105 110 115
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met
120 125 130
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg
135 140 145
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca
 1027
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg
 1075
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg
 1123
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat
 1171
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat
 1219
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg
 1267
 Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp
 375 380 385



att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa
 1315
 Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys
 390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa
 1363
 Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu
 410 415 420

gtc tagaaaaatc cagctagacc act
 1389
 Val

<210> 626
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 626
 Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val
 1 5 10 15
 Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val
 20 25 30
 Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu
 35 40 45
 Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
 50 55 60
 Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
 65 70 75 80
 Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
 85 90 95
 Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
 100 105 110
 Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
 115 120 125
 Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
 130 135 140
 Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
 145 150 155 160
 Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
 165 170 175
 Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
 180 185 190
 Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
 195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627

<211> 1092

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1069)

<223> RXA00581

<400> 627

gcacgtggtt actcacgtgc ccacgtcttt tagccaccca ttgaagtga aaaataaccc 60

 cgatcacact agtggagtag ctaaggtgca caatggattc atg gca gag caa aac 115
 Met Ala Glu Gln Asn

1

5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc 163
 Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe
 10 15 20

agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac 211
 Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn
 25 30 35

tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc 259
 Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly
 40 45 50

atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg 307
 Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro
 55 60 65

ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act 355
 Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr
 70 75 80 85

gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg 403
 Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro
 90 95 100

ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc 451
 Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr
 105 110 115

gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc 499
 Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg
 120 125 130

gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta 547
 Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu
 135 140 145

atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac 595
 Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp
 150 155 160 165

caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc 643
 Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu
 170 175 180

gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca 691
 Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro
 185 190 195

ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc 739
 Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly
 200 205 210

tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc 787
 Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe
 215 220 225

gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg 835
 Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp
 230 235 240 245

tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc 883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
 250 255 260
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
 265 270 275
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
 280 285 290
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa
 1027
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
 295 300 305
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc
 1069
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
 310 315 320
 taggggttct tgctggtttt gag
 1092

<210> 628

<211> 323

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 628

Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro
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 Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp
 20 25 30
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175
 Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190
 Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205
 Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220
 Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240
 Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255
 Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270
 Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285
 Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
 290 295 300
 Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
 305 310 315 320
 Arg Lys Ile

<210> 629
 <211> 1023
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXS00838

<400> 629
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 tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
 Met Lys Ile Ala Ile
 1 5
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20
 tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
 25 30 35
 ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40	45	50	
gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat			307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp			
55	60	65	
gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct			355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala			
70	75	80	85
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag			403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln			
	90	95	100
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat			451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Lys Ser Ile Gly Ala Asp			
	105	110	115
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca			499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro			
	120	125	130
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat			547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp			
	135	140	145
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt			595
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly			
150	155	160	165
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa			643
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys			
	170	175	180
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag			691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys			
	185	190	195
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg			739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu			
	200	205	210
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg			787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro			
	215	220	225
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag			835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu			
230	235	240	245
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt			883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser			
	250	255	260
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg			931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val			
	265	270	275
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg			979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu			
	280	285	290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg

1023

Lys Glu Glu Glu Asn Ser Leu
295 300

<210> 630

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 630

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
245 250 255



Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
 260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
 275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Asn Ser Leu
 290 295 300

<210> 631
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

<400> 631
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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac 408

<210> 632
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 632
 Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp

1	5	10	15
Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys	20	25	30
Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg	35	40	45
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe	50	55	60
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile	65	70	75
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly	85	90	95

<210> 633

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXN03058

<400> 633

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gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

105	110	115	
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata			499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile			
120	125	130	
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga			547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly			
135	140	145	
atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc			593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro			
150	155	160	
tataaaccaa aaa			606

<210> 634

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 634

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
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Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
145 150 155 160

Pro

<210> 635

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(583)

<223> FRXA02903

<400> 635

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gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
 150 155 160

tataaaccaa aaa 606

<210> 636

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
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 Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30
 Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
 35 40 45
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140
 Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160
 Pro

<210> 637

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXA00166

<400> 637

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 gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115
 Val Glu Leu Ala Arg
 1 5
 ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20
 agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35
 atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala	Val	Pro	Cys	Trp	Gln		
		40					45					50					
gcg	aca	gca	gaa	cac	aca	gga	ata	cgt	gac	aac	gcg	gtt	gat	ctg	att	307	
Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	Ala	Val	Asp	Leu	Ile		
	55					60					65						
acg	tgc	gca	caa	acg	tgg	cat	tgg	gtt	gac	gtg	acg	gct	gcc	tca	gcg	355	
Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	Thr	Ala	Ala	Ser	Ala		
	70				75					80					85		
gaa	ttt	gat	cgg	gtg	att	gca	cct	gag	ggc	gca	gtc	ctg	ctc	gtg	tgg	403	
Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	Val	Leu	Leu	Val	Trp		
				90				95						100			
aat	aac	ctg	gac	acc	tcc	atc	gcg	tgg	gta	cac	cga	ctc	agt	cgc	att	451	
Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	Arg	Leu	Ser	Arg	Ile		
		105					110						115				
atg	cat	gcc	ggc	gat	gta	ctc	aag	ccg	gga	ttc	acc	cca	gaa	acc	gca	499	
Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	Thr	Pro	Glu	Thr	Ala		
		120				125						130					
gct	ccc	tgg	ata	att	gat	cga	gaa	att	cgc	acc	acg	tgg	aat	cag	cac	547	
Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	Thr	Trp	Asn	Gln	His		
	135					140						145					
ctc	acc	cct	gaa	gaa	atc	atc	cag	ctc	gct	cac	acg	agg	tcc	tac	tgg	595	
Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	Thr	Arg	Ser	Tyr	Trp		
	150				155					160					165		
tta	aac	gcg	tca	gag	aaa	atc	aaa	gag	cgt	gtt	gat	cag	aac	ctt	cag	643	
Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	Asp	Gln	Asn	Leu	Gln		
				170				175						180			
tgg	tat	ctc	tac	gag	cat	ttg	ggc	ttc	agt	ccc	gac	aat	cca	gtg	gaa	691	
Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	Asp	Asn	Pro	Val	Glu		
			185				190						195				
ctt	ccc	tat	cgc	tgt	gat	gca	ttt	tta	ctt	tca	cgt	tcc	ggc	acc	ctg	739	
Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	Arg	Ser	Gly	Thr	Leu		
		200				205						210					
gca	ggc	aga	tct	tcc	aat	ctt	taggagccct	cgccatgtac	ctg							783	
Ala	Gly	Arg	Ser	Ser	Asn	Leu											
	215					220											

<210> 638

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

Val	Glu	Leu	Ala	Arg	Gly	Phe	Gly	Arg	Val	Leu	Asp	Val	Gly	Ala	Gly
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Thr	Gly	Lys	Leu	Thr	Ser	Glu	Leu	Thr	Ala	Asp	Gln	Val	Leu	Ala	Leu
			20					25					30		

Asp	Pro	Ser	Met	Asp	Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45						
Val	Pro	Cys	Trp	Gln	Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	
50					55					60						
Ala	Val	Asp	Leu	Ile	Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	
65					70					75					80	
Thr	Ala	Ala	Ser	Ala	Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	
					85					90					95	
Val	Leu	Leu	Val	Trp	Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	
100					105					110						
Arg	Leu	Ser	Arg	Ile	Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	
115					120					125						
Thr	Pro	Glu	Thr	Ala	Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	
130					135					140						
Thr	Trp	Asn	Gln	His	Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	
145					150					155					160	
Thr	Arg	Ser	Tyr	Trp	Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	
					165					170					175	
Asp	Gln	Asn	Leu	Gln	Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	
180					185					190						
Asp	Asn	Pro	Val	Glu	Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	
195					200					205						
Arg	Ser	Gly	Thr	Leu	Ala	Gly	Arg	Ser	Ser	Asn	Leu					
210					215					220						

<210> 639

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXA00633

<400> 639

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tacactgcag	atatacatcc	aaaccaagtg	acggaggaaa	atg	gaa	aac	ccc	agc	115
				Met	Glu	Asn	Pro	Ser	
				1				5	

ttg	cgc	gag	ctt	gat	cac	cga	aac	atc	tgg	cac	ccg	tat	gcc	gcg	ccg	163
Leu	Arg	Glu	Leu	Asp	His	Arg	Asn	Ile	Trp	His	Pro	Tyr	Ala	Ala	Pro	
				10					15					20		

ggc	gtg	cgc	aat	aga	ctc	gtc	acc	aaa	acc	gat	gga	gtg	ttt	ttg	acg	211
Gly	Val	Arg	Asn	Arg	Leu	Val	Thr	Lys	Thr	Asp	Gly	Val	Phe	Leu	Thr	
			25					30					35			

ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg	259
Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser	
40 45 50	
gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa	307
Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys	
55 60 65	
caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag	355
Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu	
70 75 80 85	
ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc	403
Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	
90 95 100	
ttt gac cac gtc ttt tat tcc gat tgc ggc tgc gtc tca gtg gag gtc	451
Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val	
105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa	499
Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	
120 125 130	
cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc	547
Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe	
135 140 145	
acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg	595
Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp	
150 155 160 165	
aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg	643
Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg	
170 175 180	
ggg tca tgc ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	691
Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu	
185 190 195	
ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa	739
Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln	
200 205 210	
ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc	787
Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val	
215 220 225	
gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att	835
Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile	
230 235 240 245	
gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat	883
Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn	
250 255 260	
ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga	931
Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	
265 270 275	
ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta	979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
 280 285 290
 atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt
 1027
 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
 295 300 305
 atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc
 1075
 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile
 310 315 320 325
 att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa
 1123
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu
 330 335 340
 ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat
 1171
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp
 345 350 355
 gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc
 1219
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc
 1267
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg
 1315
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa
 1363
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420
 ggg aaa taaaccatgc catttttatt tgt
 1392
 Gly Lys

<210> 640

<211> 423

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
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 Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
 35 40 45
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
 50 55 60
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
 65 70 75 80
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
 85 90 95
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
 100 105 110
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
 115 120 125
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
 130 135 140
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
 145 150 155 160
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
 165 170 175
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
 180 185 190
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
 195 200 205
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
 210 215 220
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
 225 230 235 240
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
 245 250 255
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
 260 265 270
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

355 360 365

Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp
370 375 380

His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro
385 390 395 400

Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu
405 410 415

His Ala Ala Val Lys Gly Lys
420

<210> 641
<211> 795
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00632

<400> 641
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ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115
Met Pro Phe Leu Phe
1 5

gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163
Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val
10 15 20

ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211
Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys
25 30 35

cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259
Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile
40 45 50

gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307
Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp
55 60 65

cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355
Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile
70 75 80 85

cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403
Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
90 95 100

cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451
Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
105 110 115

gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499



Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130

gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145

agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165

ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180

gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195

gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210

gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220

tcg 795

<210> 642
 <211> 224
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 642
 Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
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Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30

Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45

Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60

Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80

Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95

Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110

Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125

Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
	210	215
		220

<210> 643
 <211> 1125
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00295

<400> 643
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 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115
 Met Thr Ile Pro Gly
 1 5
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly
 10 15 20
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln
 25 30 35
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys
 40 45 50
 ggg gaa gaa atc gag gtc gag ggc att att tcc ctc aaa act ggc ggt 307
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly
 55 60 65
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser
 70 75 80 85
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala
 90 95 100

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aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val
120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595
Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His
150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739
Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835
Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
1027
Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
1075
Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac
1122

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Pro Ile Lys Val Leu Asn Lys Val Ile
330

gac
1125

<210> 644
<211> 334
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 644

Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu
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Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr
20 25 30

Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val
35 40 45

Arg Leu Lys Trp Cys Gly Glu Ile Glu Val Glu Gly Ile Ile Ser
50 55 60

Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser
65 70 75 80

Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn
85 90 95

Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe
100 105 110

Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln
115 120 125

Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val
130 135 140

Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala
145 150 155 160

Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser
165 170 175

Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu
180 185 190

Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly
195 200 205

Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val
210 215 220

Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp
225 230 235 240

Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr
 260 265 270
 Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly
 275 280 285
 Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn
 290 295 300
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met
 305 310 315 320
 Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile
 325 330

<210> 645
 <211> 1212
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1189)
 <223> RXA00223

<400> 645
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 tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115
 Met Arg Glu Val Ala
 1 5
 gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln
 10 15 20
 tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu
 25 30 35
 gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr
 40 45 50
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His
 55 60 65
 gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly
 70 75 80 85
 att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu
 90 95 100
 ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tgc gcc tgc tcc aac ggt gta aac
 1027
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc
 1075
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc
 1123
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg
 1212
 Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
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Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu



	245							250							255													
His Thr Ile Pro Asn Val Leu Val His Thr Thr Glu Pro Ser Leu Pro																												
	260							265							270													
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile																												
	275							280							285													
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys																												
	290							295							300													
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile																												
305	310							315							320													
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr																												
	325							330							335													
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val																												
	340							345							350													
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe																												
	355							360																				
<210>	647																											
<211>	1197																											
<212>	DNA																											
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<222>	(101)..(1174)																											
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	Met Leu Tyr Leu Asp 1 5																											
aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg	163																											
Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp	10 15 20																											
cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg	211																											
Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val	25 30 35																											
gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc	259																											
Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala	40 45 50																											
cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga	307																											
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly	55 60 65																											
tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct	355																											
Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro	70 75 80 85																											

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta 403
 Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 90 95 100

gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac 451
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 105 110 115

cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa 499
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 120 125 130

gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat 547
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 135 140 145

gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt 595
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 150 155 160 165

acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac 643
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 170 175 180

ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct 691
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 185 190 195

aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc 739
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 200 205 210

cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt 787
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 215 220 225

gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa 835
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 230 235 240 245

tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg 883
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 250 255 260

gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca 931
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 265 270 275

tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg 979
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 280 285 290

gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga
 1027
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 295 300 305

gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca
 1075
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 310 315 320 325

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 210 215 220
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 225 230 235 240
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 245 250 255
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 260 265 270
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 275 280 285
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 290 295 300
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 305 310 315 320
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 325 330 335
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 340 345 350
 Val Ala Leu Ile Arg Gly
 355

<210> 649
 <211> 920
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (79)..(897)
 <223> FRXA00262

<400> 649
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 cgtgcttagc taatcctagt gcc ggg cac ctc atc acc acc ccg atc gag 111
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
 1 5 10
 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 15 20 25
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 30 35 40
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 45 50 55

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ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt 495
Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagagggttta cgg 920
Val Ala Leu Ile Arg Gly
270

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<210> 650

<211> 273

<212> PRT

<213> Corynebacterium glutamicum



<400> 650

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 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 20 25 30
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 35 40 45
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 245 250 255
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 260 265 270

Gly

<210> 651

<211> 1296

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1273)

<223> RXN00435

<400> 651

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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
                               Val Gly Phe Asp Val
                               1                               5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
                               10                               15                               20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
                               25                               30                               35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
                               40                               45                               50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
                               55                               60                               65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70                               75                               80                               85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
                               90                               95                               100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
                               105                               110                               115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
                               120                               125                               130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
135                               140                               145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
150                               155                               160                               165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
                               170                               175                               180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
                               185                               190                               195

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ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc
 1027
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc
 1075
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac
 1123
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca
 1171
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg
 1219
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg
 1267
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc
 1296
 Leu Ala
 390

<210> 652

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 652

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
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 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140
 Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
 145 150 155 160
 His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
 165 170 175
 Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
 180 185 190
 Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
 195 200 205
 Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
 210 215 220
 Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
 225 230 235 240
 Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
 245 250 255
 Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
 260 265 270
 Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
 275 280 285
 His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
 290 295 300

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
 305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
 325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
 340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
 355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
 370 375 380

Arg Val Leu Ala Ser Leu Ala
 385 390

<210> 653
 <211> 638
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(615)
 <223> FRXA00435

<400> 653

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Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg	96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	



115	120	125	
ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc acc atg gaa ggc gtg			432
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135	140	
ccc gca gat atg gtg tac cgc cga ttg gtg gac aat cgt ttg atc act			480
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160
acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa			528
Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu			
	165	170	175
gct ggc gga tcg atc act atc gga cta agc ccg ttt agc acc tac tat			576
Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr			
	180	185	190
gaa gtg gat cag ctg acc agg gtg ctg gca tcg ctt gcc taaaccgcaa			625
Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala			
195	200	205	
gcacgagctt gcc			638
 <210> 654			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 654			
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Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro			
	20	25	30
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu			
	35	40	45
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly			
	50	55	60
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp			
	65	70	75
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe			
	85	90	95
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His			
	100	105	110
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala			
	115	120	125
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
	130	135	140
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
	145	150	155
			160

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
180 185 190

Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
195 200 205

<210> 655

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02801

<400> 655

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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
Val Gly Phe Asp Val
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

135 140 145

<210> 656
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 656
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 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140
 Gln
 145

<210> 657
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1363)
 <223> RXA02516

<400> 657
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 aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115
 Met Ser Asp Phe Leu
 1 5
 aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
 10 15 20

atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac	211
Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp	
25 30 35	
tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr
 265 270 275

gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
 280 285 290

gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg
 1027
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
 295 300 305

gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa
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 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
 310 315 320 325

aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca
 1123
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
 330 335 340

gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca
 1171
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
 345 350 355

cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc
 1219
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
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ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg
 1267
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
 375 380 385

aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac
 1315
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
 390 395 400 405

cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag
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 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
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 1386

<210> 658
 <211> 421
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 658
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 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

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Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His															
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Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr															
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Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln															
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Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr															
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Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala															
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Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu															
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Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu															
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Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val															
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Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly
 355 360 365
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser
 370 375 380
 Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr
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 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln
 405 410 415
 Phe Phe Gly Val Glu
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 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(547)
 <223> RXA02517

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 Met Asn Leu Glu Gln
 1 5
 atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys
 10 15 20
 ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser
 25 30 35
 tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259
 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser
 40 45 50
 acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307
 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln
 55 60 65
 gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp
 70 75 80 85
 aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg
 90 95 100
 ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
 120 125 130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His
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<210> 660
 <211> 149
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 660
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Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His
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His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
 50 55 60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
 130 135 140

Val Ala His Ala His
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<210> 661
 <211> 1167
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1144)
 <223> RXA01747

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ctaaaaatat cactaactcg aaagatgtaa ggttgcattt	gtg act atc gca cct	115
	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
10 15 20		
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
25 30 35		
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
40 45 50		
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
55 60 65		
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
70 75 80 85		
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
90 95 100		
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
105 110 115		
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
120 125 130		
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
135 140 145		
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
150 155 160 165		
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
170 175 180		
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
185 190 195		
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
200 205 210		
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
215 220 225		



acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
 230 235 240 245

 atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
 250 255 260

 tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu
 265 270 275

 atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
 280 285 290

 cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa
 1027
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

 atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc
 1075
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
 310 315 320 325

 gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac
 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

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 Thr Pro Val Val Ser Phe Asn
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<210> 662

<211> 348

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 662

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 20 25 30

 Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45

 Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

 Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
 195 200 205
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
 210 215 220
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
 260 265 270
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
 275 280 285
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
 290 295 300
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
 305 310 315 320
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
 325 330 335
 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
 340 345

<210> 663

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(853)

<223> RXA01746

<400> 663

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	Met Thr Ala Pro Arg	
	1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163	
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro		
10 15 20		
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211	
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp		
25 30 35		
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259	
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp		
40 45 50		
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307	
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg		
55 60 65		
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355	
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala		
70 75 80 85		
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403	
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile		
90 95 100		
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451	
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val		
105 110 115		
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499	
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val		
120 125 130		
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547	
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala		
135 140 145		
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595	
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile		
150 155 160 165		
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643	
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr		
170 175 180		
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691	
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly		
185 190 195		
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739	
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu		
200 205 210		
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787	
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg		
215 220 225		

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
 250

<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg
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Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly



245

250

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<211> 1179
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1156)  
<223> RXA02106
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Met Asn Asn His Phe																5
1																
gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc																163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr																20
10 15																
gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc																211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu																35
25 30																
gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg																259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala																50
40 45																
tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg																307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala																65
55 60																
ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat																355
Leu Ala Glu Tyr Asp Asn Val Glu Leu His Gly Phe Ser Thr Ala Asp																85
70 75 80																
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Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr																100
90 95																
gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt																451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu																115
105 110																
aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag																499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln																130
120 125																
cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg																547
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val																145
135 140																
atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt																595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val																165
150 155 160																
aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt gcc ggt gca																643

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				170					175					180			
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Met	Phe	Met	Glu	Gly	Gly	Asn	Cys	Ile	Thr	Tyr	Ser	Leu	Tyr	Ala	Pro		
			185					190					195				
gaa	tct	ctc	gtt	gct	ggc	ttg	agc	tat	gag	cag	tcc	tat	gaa	tat	ttg	739	
Glu	Ser	Leu	Val	Ala	Gly	Leu	Ser	Tyr	Glu	Gln	Ser	Tyr	Glu	Tyr	Leu		
		200					205					210					
gat	cgt	tgg	gtg	att	gct	gcg	ctg	aag	aca	cac	gat	gtt	gac	gct	tgg	787	
Asp	Arg	Trp	Val	Ile	Ala	Ala	Leu	Lys	Thr	His	Asp	Val	Asp	Ala	Trp		
	215					220					225						
tac	gtg	cct	atc	aat	gac	atc	acc	tcc	acc	ggc	gga	aaa	atc	ggc	ggc	835	
Tyr	Val	Pro	Ile	Asn	Asp	Ile	Thr	Ser	Thr	Gly	Gly	Lys	Ile	Gly	Gly		
230					235					240				245			
gct	gca	cag	aaa	cgt	cgc	agt	ggc	gca	gtc	ctc	cac	cac	gtg	acc	atg	883	
Ala	Ala	Gln	Lys	Arg	Arg	Ser	Gly	Ala	Val	Leu	His	His	Val	Thr	Met		
				250				255						260			
tcc	tat	gac	atc	gat	gcg	gac	atg	atg	acc	cag	gtg	ttg	cgc	att	gga	931	
Ser	Tyr	Asp	Ile	Asp	Ala	Asp	Met	Met	Thr	Gln	Val	Leu	Arg	Ile	Gly		
			265				270						275				
aag	gtg	aag	att	tcc	gac	aag	ggc	ctt	cgc	agc	gca	aag	aag	cgc	gtt	979	
Lys	Val	Lys	Ile	Ser	Asp	Lys	Gly	Leu	Arg	Ser	Ala	Lys	Lys	Arg	Val		
		280					285					290					
gat	cct	ctg	cgc	cgc	caa	aca	ggc	gca	tca	cgt	gag	caa	atc	atc	gac		
1027																	
Asp	Pro	Leu	Arg	Arg	Gln	Thr	Gly	Ala	Ser	Arg	Glu	Gln	Ile	Ile	Asp		
	295					300					305						
acc	cta	aag	tcc	aca	ttc	agt	gct	agg	tac	ggc	gcg	caa	gaa	gta	gag		
1075																	
Thr	Leu	Lys	Ser	Thr	Phe	Ser	Ala	Arg	Tyr	Gly	Ala	Gln	Glu	Val	Glu		
310					315					320					325		
ctc	agc	gat	gaa	gat	ttc	gcg	gca	ggc	cac	gac	cta	gta	aaa	acc	aaa		
1123																	
Leu	Ser	Asp	Glu	Asp	Phe	Ala	Ala	Gly	His	Asp	Leu	Val	Lys	Thr	Lys		
				330					335					340			
tac	gcc	acc	gag	gag	tgg	act	aag	cga	gtt	caa	tag	ttt	ctat	ggat	ctgcac		
1176																	
Tyr	Ala	Thr	Glu	Glu	Trp	Thr	Lys	Arg	Val	Gln							
			345					350									
aag																	
1179																	

<210> 666

<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
 1 5 10 15
 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
 20 25 30
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
 35 40 45
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
 50 55 60
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
 65 70 75 80
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
 85 90 95
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
 165 170 175
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
 245 250 255
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
 260 265 270
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
 275 280 285
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
 290 295 300
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
 305 310 315 320
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325

330

335

Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
 340 345 350

<210> 667

<211> 403

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(403)

<223> RXS01183

<400> 667

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 ttccgtttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115
 Met Ala Phe Ser Val
 1 5
 gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163
 Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln
 10 15 20
 tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211
 Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu
 25 30 35
 gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259
 Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala
 40 45 50
 ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307
 Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val
 55 60 65
 ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355
 Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn
 70 75 80 85
 gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403
 Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro
 90 95 100

<210> 668

<211> 101

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 668

Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu
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 Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

20 25 30
 Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile
 35 40 45
 Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp
 50 55 60
 Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp
 65 70 75 80
 Glu Thr Pro Ala Asn Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala
 85 90 95
 Glu Glu Glu Glu Pro
 100

<210> 669
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXS01260

<400> 669
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 ctttaccatc gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
 Val Thr Phe Asn Tyr
 1 5
 gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
 10 15 20
 ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
 25 30 35
 ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
 40 45 50
 gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
 55 60 65
 tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
 70 75 80 85
 tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
 90 95 100
 att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

105					110					115					
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt	499														
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu															
120 125 130															
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag	547														
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys															
135 140 145															
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg	595														
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg															
150 155 160 165															
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643														
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp															
170 175 180															
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691														
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe															
185 190 195															
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739														
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu															
200 205 210															
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787														
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val															
215 220 225															
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835														
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala															
230 235 240 245															
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883														
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly															
250 255 260															
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931														
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr															
265 270 275															
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979														
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala															
280 285 290															
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc															
1027															
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe															
295 300 305															
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca															
1075															
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala															
310 315 320 325															
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg															
1123															
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu															
330 335 340															



gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag
 1171
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
 345 350 355

 aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac
 1219
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
 360 365 370

 cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga
 1267
 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
 375 380 385

 cac atg atc aac ttc tagaatccac ctcggttgcc ctg
 1305
 His Met Ile Asn Phe
 390

 <210> 670
 <211> 394
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 670
 Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
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 Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
 20 25 30

 Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
 35 40 45

 Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
 50 55 60

 Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
 65 70 75 80

 Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
 85 90 95

 Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
 100 105 110

 Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
 115 120 125

 Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
 130 135 140

 Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
 145 150 155 160

 Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
 165 170 175

 Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180					185					190					
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225					230					235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
				245					250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
			260					265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val
	290					295					300				
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu
305					310					315					320
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu
				325					330					335	
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu
			340					345					350		
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg
		355					360					365			
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala
	370					375					380				
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe						
385					390										

<210> 671

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXS01261

<400> 671

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				Val	Thr	Glu	His	Tyr	
				1				5	

gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggt	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
	55			

<210> 672

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly	
1 5 10 15	

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val	
20 25 30	

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile	
35 40 45	

Pro Ser Lys Val Ser Asp Gln Lys Arg	
50 55	

<210> 673

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02717

<400> 673

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gcgtccttca cccggccgag tacctttttc tgtcgagttt atg cca ccc cgc gac	115
Met Pro Pro Arg Asp	
1 5	

gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
10 15 20	

ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
25 30 35	

cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu	

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg 307 Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met 55 60 65			
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg 355 Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu 70 75 80 85			
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc 403 Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 90 95 100			
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag 451 Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys 105 110 115			
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc 499 Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro 120 125 130			
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act 547 Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr 135 140 145			
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc 595 Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe 150 155 160 165			
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca 643 Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala 170 175 180			
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att 691 Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile 185 190 195			
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa 739 Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln 200 205 210			
ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat 787 Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn 215 220 225			
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc 835 Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser 230 235 240 245			
acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac 883 Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His 250 255 260			
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac 931 Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn 265 270 275			
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg 979 Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val 280 285 290			

cgt taagccctct taggaatcat gaa
 1005
 Arg

<210> 674
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 674

Met	Pro	Pro	Arg	Asp	Asp	Ala	Ala	Glu	Glu	Arg	Leu	Tyr	Arg	Ala	Ala	1	5	10	15
Glu	Val	Phe	His	Asp	Leu	Gly	Ala	Ser	Phe	Val	Ser	Val	Thr	Tyr	Gly	20	25	30	
Ala	Gly	Gly	Ser	Thr	Arg	Glu	Arg	Thr	Ser	Arg	Ile	Ala	Arg	Arg	Leu	35	40	45	
Ala	Lys	Gln	Pro	Leu	Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Asn	His	50	55	60	
Thr	Arg	Glu	Glu	Met	Lys	Ala	Ile	Leu	Arg	Glu	Tyr	Leu	Glu	Leu	Gly	65	70	75	80
Leu	Thr	Asn	Leu	Leu	Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Leu	85	90	95	
Gly	Asp	Trp	Val	Ser	Thr	Asp	Gly	Gly	Leu	Asn	Tyr	Ala	Ser	Glu	Leu	100	105	110	
Ile	Asp	Leu	Ile	Lys	Ser	Thr	Pro	Glu	Phe	Arg	Glu	Phe	Asp	Leu	Gly	115	120	125	
Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Phe	Arg	Ala	Lys	Thr	Leu	Glu	Glu	130	135	140	
Asp	Thr	Lys	Tyr	Thr	Leu	Ala	Lys	Leu	Arg	Gly	Gly	Ala	Glu	Tyr	Ser	145	150	155	160
Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Glu	Asp	Tyr	Leu	Arg	Leu	Arg	Asp	165	170	175	
Arg	Leu	Val	Ala	Ala	Asp	Pro	Ile	His	Gly	Ala	Lys	Pro	Ile	Ile	Pro	180	185	190	
Gly	Ile	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Val	Glu	195	200	205	
Leu	Ser	Gly	Ala	Gln	Leu	Pro	Ser	Gln	Leu	Glu	Glu	Ser	Leu	Val	Arg	210	215	220	
Ala	Ala	Asn	Gly	Asn	Glu	Glu	Ala	Asn	Lys	Asp	Glu	Ile	Arg	Lys	Val	225	230	235	240
Gly	Ile	Glu	Tyr	Ser	Thr	Asn	Met	Ala	Glu	Arg	Leu	Ile	Ala	Glu	Gly	245	250	255	

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
 260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
 275 280 285

Gly Gln Asp Ala Val Arg
 290

<210> 675
 <211> 601
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(601)
 <223> RXN02027

<400> 675
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tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135 140 145
 gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

 gat atc 601
 Asp Ile

<210> 676
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15

 Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45

 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60

 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80

 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95

 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110

 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125

 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140

 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160

 Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> FRXA02027

<400> 677

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtacc cctccgaaaa taacgggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala



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<210> 679
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00106
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951

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
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 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150



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<210> 681
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1021)  
<223> RXN01321
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<400> 681
ggagggtgta gtcaaggatt tgggccatgg tggagcggga aatcgtcata tccataccct 60

acttagacct gacttagtgt gggaaaattt ccagggtaga atg caa cga atg acc 115
Met Gln Arg Met Thr
1 5

ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163
 Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu
 10 15 20

cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val
25 30 35

gcg aag ttg tgc tgc ttc cta gct gag cgt ggg ggt tgg att act gag 259
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu
40 45 50

gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag 307
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln
55 60 65

gcg att cgc gct gag tcg att gat acc acg att gag cag ttg cgg gag 355
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu
70 75 80 85

gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser
90 95 100

ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys
105 110 115

gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp
120 125 130

tat	ccg	atg	gaa	gtt	gtt	gcg	gtt	gtg	ggt	aac	cat	gag	aac	ttg	cgt	547
Tyr	Pro	Met	Glu	Val	Val	Ala	Val	Val	Gly	Asn	His	Glu	Asn	Leu	Arg	
	135					140					145					

tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct	595
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro	
150	155
	160
	165

aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile
170 175 180


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gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag      691
Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln
      185                                190                                195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat      739
Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
      200                                205                                210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat      787
Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
      215                                220                                225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat      835
Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
      230                                235                                240                                245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att      883
Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
      250                                255                                260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc      931
Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
      265                                270                                275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag      979
Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
      280                                285                                290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
1021
Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
      295                                300                                305

taaggctttt tgcttttcga cgc
1044

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<210> 682

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 682

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Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser
  1                                5                                10                                15

Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp
      20                                25                                30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
      35                                40                                45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
      50                                55                                60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
      65                                70                                75                                80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
      85                                90                                95

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Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
 305

<210> 683

<211> 582

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (23)..(559)

<223> FRXA01321

<400> 683

cttgcacgat ttgttaggtc gtgtg gct gag aat gat tat ccg atg gaa gtt 52
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val
 1 5 10
 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
 30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
 45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
 60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
 75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
 95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
 110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
 125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
 140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
 155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
 175

cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 1 5 10 15

His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
165 170 175

Val Phe Asp

<210> 685
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00461

<400> 685
tggtgggagg gatgacagga ttgtcgaaga taacgtgaag tgggtgttcc ggcattgtgtt 60

tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115
Val Thr Ala Ile Lys
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct				403
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro				
	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag				451
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys				
	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac				499
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn				
	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg				547
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu				
	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc				595
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly				
	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt				643
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg				
	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg				691
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu				
	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag				739
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln				
	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc				787
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu				
	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac				835
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His				
	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc				883
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly				
	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc				931
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg				
	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg				975
Ala Glu Lys Leu Ala Gly Leu				
	280			

<210> 686

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe
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 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val
 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

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accacagaaa tgcctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtcgcgt 60
gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
Val Asp Asn His Ala
1 5
gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
10 15 20
ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
25 30 35
acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
40 45 50
cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
55 60 65
gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
70 75 80 85
cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
90 95 100
ggg aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
105 110 115
gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
120 125 130
att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
135 140 145
gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
150 155 160 165
cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
170 175 180
aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
185 190 195
taaataaacg taccctcttt gac 711

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<210> 688
 <211> 196
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 688
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 Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
 20 25 30
 Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
 35 40 45
 Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60
 Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80
 Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95
 Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110
 Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
 115 120 125
 Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
 130 135 140
 Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
 145 150 155 160
 Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
 165 170 175
 Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
 180 185 190
 Ile Arg Gly His
 195

<210> 689
 <211> 513
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(490)
 <223> RXA01516

<400> 689
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<210> 690
<211> 130
<212> PRT
<213> Corynebacterium glutamicum
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<400> 690																
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1				5					10					15		
Gly	Val	Phe	Asp	Phe	Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp	
			20					25					30			
Val	Thr	Cys	Trp	Met	Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu	
		35					40					45				
Ser	Asp	Thr	Val	Asp	Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile	
	50					55					60					
Val	Glu	Gly	Pro	Ser	Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser	
65					70					75					80	
Ala	Asp	Ala	Val	Met	Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val	
				85					90					95		

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 691
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(952)
 <223> RXA01515

<400> 691
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ctccccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 692

<211> 284

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 692

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 20 25 30
 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

965

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694
 <211> 253
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 694

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Ser	Phe	Tyr	Asp	Lys	Gly	Ala	Thr	Phe	Glu	Asp	Thr	Ala	Ala	Leu	Asn
			20					25					30		
Arg	Ala	Ala	Glu	Val	Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly
	35					40						45			
Gly	Val	Lys	Ala	Gly	Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile
	50					55					60				
Asp	Arg	Val	Val	Pro	Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp
65					70					75				80	
Ile	Asp	Ile	Ser	Val	Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala
				85					90					95	
Val	Ala	His	Gly	Ala	Thr	Leu	Ile	Asn	Asp	Thr	Trp	Ala	Gly	His	Asp
			100					105					110		
His	Glu	Leu	Val	Gln	Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys
	115						120					125			
Ser	His	Thr	Gly	Gly	Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His
	130					135					140				
Phe	Asp	Asp	Ile	Val	Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala
145					150					155				160	
Glu	Gln	Ala	Val	Arg	Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp
			165					170					175		
Pro	Thr	His	Asp	Phe	Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu
		180						185					190		
Arg	Arg	Ile	Asp	Glu	Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala
		195					200					205			
Leu	Ser	Asn	Lys	Asp	Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp
	210					215					220				
Lys	Arg	Val	Ala	Gly	Thr	Leu	Ala	Ala	Thr	Ala	Trp	Ala	Ala	Ala	Arg
225				230					235						240
Gly	Val	Ala	Ala	Phe	Arg	Val	His	Glu	Val	Ala	Glu	Thr			
			245					250							

<210> 695
 <211> 579
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(556)
 <223> RXA00106

<400> 695

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
                                   Met Ile Gly Ala Ile
                                   1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                                   10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                                   25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                                   40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                                   55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
                                   70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                                   90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                                   105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                                   120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
                                   135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

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<210> 696
 <211> 152
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 696

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  1 5 10 15

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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 697

<211> 1556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1533)

<223> RXA00989

<400> 697

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 1 5 10 15
 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala



325	330	335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca		
1056		
Ala Leu Ala	Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro	
340	345	350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca		
1104		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro		
355	360	365
ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca		
1152		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala		
370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt		
1200		
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg		
385	390	395
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac		
1248		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp		
405	410	415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa		
1296		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu		
420	425	430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat		
1344		
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp		
435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc		
1392		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val		
450	455	460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa		
1440		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu		
465	470	475
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc		
1488		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile		
485	490	495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca		
1533		
Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala		
500	505	510
tgagcaagcg tgaagaatca att		
1556		

<400> 698

Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
20 25 30

Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
50 55 60

Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
65 70 75 80

Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala
85 90 95

Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile
100 105 110

Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser
115 120 125

Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro
130 135 140

Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr
145 150 155 160

Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met
165 170 175

Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp
180 185 190

Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp
195 200 205

Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val
210 215 220

Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala
225 230 235 240

Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly
245 250 255

Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu
260 265 270

Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val
275 280 285

972



973

	10	15	20	
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
	150	155		
gca				600
<210> 700				
<211> 159				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 700				
Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala				
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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln				
	20	25	30	
Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu				
	35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu				
	50	55	60	
Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg				
	65	70	75	80



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<210> 701
<211> 1983
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1960)
<223> RXA00579
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gtgcttttct cgttgttttg tggttttgtc agaggatgtc																
Met Arg Val Leu Ile																115
1 5																
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa																163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu																
10 15 20																
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata																211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile																
25 30 35																
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac																259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His																
40 45 50																
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt																307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg																
55 60 65																
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg																355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala																
70 75 80 85																
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt																403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly																
90 95 100																
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc																451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile																
105 110 115																

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
 Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
 120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
 Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
 135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
 Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
 150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
 215 220 225

ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc 835
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa
 1027
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt
 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct
 1123
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
 1315
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
 1363
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc
 1411
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa
 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
 1507
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc
 1555
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca
 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 702

<211> 620

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
 130 135 140
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
 145 150 155 160
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
 165 170 175
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
 180 185 190
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
 195 200 205
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450	455	460
Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala		
465	470	475 480
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val		
	485	490 495
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu		
	500	505 510
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly		
	515	520 525
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp		
	530	535 540
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr		
	545	550 555 560
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu		
	565	570 575
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu		
	580	585 590
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser		
	595	600 605
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro		
	610	615 620

<210> 703

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 703

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ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 50

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cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
    55                60                65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
    70                75                80                85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                90                95                100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                105                110                115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
                120                125                130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
    135                140                145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
    150                155                160                165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                170                175                180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                185                190                195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
    200                205

tca 747

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<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

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Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
                20                25                30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
                35                40                45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
    50                55                60

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Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
195 200 205

<210> 705
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXA02790

<400> 705
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agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
Met Glu Pro Val Tyr
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu	
55 60 65	
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc	355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
70 75 80 85	
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gcag gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
1027
Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
1075
Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
1123
Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
1171
Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
1219
Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg
1266
Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 706
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 706
Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr
1 5 10 15
Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
20 25 30
Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala
100 105 110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

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<210> 708
<211> 152
<212> PRT
<213> Corynebacterium glutamicum
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986

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Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
145 150

<210> 709

<211> 2599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2599)

<223> RXN02198

<400> 709

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agttcgggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115
Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct			451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala			
105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt			499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly			
120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat			547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr			
135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac			595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp			
150	155	160	165
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag			643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln			
170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat			691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp			
185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc			739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr			
200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca			787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro			
215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag			835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu			
230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg			883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val			
250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca			931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala			
265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc			979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe			
280	285	290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca			
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr			
295	300	305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag			
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu			
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cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
 1123
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
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gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385

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 1315
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
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 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
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gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
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 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
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 1459
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
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gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
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 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
 455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
 1555
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
 1603
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
 490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
 1651
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
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gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
 1699
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 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
 1795
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
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gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
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 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
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cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
 1891
 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
 585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
 1939
 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
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 1987
 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
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tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
 2035
 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
 630 635 640 645

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 2083
 Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
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cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
 2131
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
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 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
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 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
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 2323
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 730 735 740

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 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

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 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

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 2563
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 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
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 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
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 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

725	730	735
Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly		
740	745	750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys		
755	760	765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser		
770	775	780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser		
785	790	800
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Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser		
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Asp

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 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
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 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
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tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
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Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
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Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
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gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
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1027	
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
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 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355

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 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
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 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
 585 590 595

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 1939
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 695 700 705

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Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
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 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
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 515 520 525
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 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
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 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
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 705 710 715 720
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Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser					
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785					790					795					800					
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															Met Thr Ser Asn Phe					
															1 5					
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg																				163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu																				
10 15 20																				
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa																				211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu																				
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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu																				
40 45 50																				
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala																				
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp																				
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg																				
90 95 100																				

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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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 345 350 355
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 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
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 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
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 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
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 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys

520	525	530
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ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795		
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550 555 560 565		
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843		
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570 575 580		
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Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg 585 590 595		
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Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600 605 610		
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Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp 630 635 640 645		
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083		
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Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val 665 670 675		
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179		
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680 685 690		
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227		
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695 700 705		
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Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710 715 720 725		

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2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
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2358

Gly Ala Thr Ile
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<212> PRT

<213> *Corynebacterium glutamicum*

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

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Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly						
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Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu						
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Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly						
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Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys						
	290		295			300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu						
305		310		315		320
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val						
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Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu						
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Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala						
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Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro						
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Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg						
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Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr						
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Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala						
	420		425			430
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met						
	435		440			445
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu						
	450		455			460
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr						
465		470		475		480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val						
	485		490			495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn						
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Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln						
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Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr						
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Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr						
545		550		555		560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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<223> FRXA02085

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Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

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atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp 70 75 80 85			355
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg 90 95 100			403
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met 105 110 115			451
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser 120 125 130			499
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu 135 140 145			547
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cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro 170 175 180			643
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys 185 190 195			691
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ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly 230 235 240 245			835
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly 250 255 260			883
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly 265 270 275			931

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 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
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ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
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 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
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 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

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 1267
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 375 380 385

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 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
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aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
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 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545
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 1795
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 550 555 560 565
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 1843
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 570 575 580
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 Arg Arg Arg
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 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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<223> FRXA02086
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Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
      25      30      35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc° aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
      40      45      50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
      55      60      65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
      70      75      80      85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
      90      95      100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
      105      110      115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
      120      125      130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
      135      140      145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
      150      155      160

aac 603

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<210> 718

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
      20      25      30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35      40      45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
      50      55      60

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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 719
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1303)
 <223> RXN02648

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 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu	
				90					95					100		
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp	
			105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser	
		120					125					130				
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly	
	135					140					145					
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu	
150					155					160					165	
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
				170					175					180		
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200					205					210				
tac	aag	atc	atc	acc	gat	gca	ggc	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys	
230					235					240				245		
gat	tac	ttg	gac	tgg	atc	ggc	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala	
				250					255					260		
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly	
			265					270					275			
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	gac	atc	att	979
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile	
		280					285					290				
ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	gaa	ggc	gca	
1027																
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala	
	295					300					305					
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt	
1075																
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu	
310					315					320					325	

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
390 395 400

aacgagggtt gct
1326

<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

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20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 721

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 721

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35           40           45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50           55           60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
        65           70           75           80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85           90           95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100          105          110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115          120          125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130          135          140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145          150          155          160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165          170          175

taagctagac aacgagggtt gct 548

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<210> 722

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

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Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 723

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 723

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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 724

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

65	70	75	80
Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg	85	90	95
Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu	100	105	110
Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr	115	120	125
Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn	130	135	140
Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln	145	150	155
Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr	165	170	175
Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr	180	185	190
Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp	195	200	205
Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val	210	215	220
Gln Leu Asp Ala			
225			

<210> 725

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXS02197

<400> 725

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ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac	96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp	
20 25 30	
ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct	144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro	
35 40 45	
att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag	192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu	
50 55 60	
tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc	240

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175
 taacaccttt gagaggaaa act 551

<210> 726

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
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 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

130		135		140
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser				
145		150		155
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val				
	165		170	175

<210> 727
 <211> 546
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(523)
 <223> RXC00988

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 Met Ser Lys Arg Glu
 1 5
 gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20
 gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35
 gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50
 gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65
 gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85
 atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100
 gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115
 gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
 120 125 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728
 <211> 141
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 728
 Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
 1 5 10 15
 His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
 20 25 30
 Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45
 Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60
 Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 729
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> RXC01518

<400> 729
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 tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
 Val Ala Phe Met Gln
 1 5
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
 90 95 100
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115
 gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
 120 125 130
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
 135 140 145
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc 594
 Pro Pro Gln Ser Gly Glu Ala Ile Ser
 150 155
 aag 597

<210> 730

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 730

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
 1 5 10 15
 Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
 20 25 30
 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45
 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60
 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80
 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
 145 150 155

<210> 731
 <211> 723
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXC01942

<400> 731
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gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
 Met Leu Arg Ile Gly
 1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
 10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
 25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
 40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
 55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
 70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
 90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
 105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp

120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc			547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu			
135	140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac			595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp			
150	155	160	165
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta			643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu			
	170	175	180
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt			691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser			
	185	190	195
cgc gtg aat tagcactaaa acatcgtcaa agt			723
Arg Val Asn			
200			

<210> 732

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr			
1	5	10	15
Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp			
	20	25	30
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu			
	35	40	45
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu			
	50	55	60
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr			
	65	70	75
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala			
	85	90	95
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr			
	100	105	110
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu			
	115	120	125
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val			
	130	135	140
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser			
	145	150	155
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp			
	165	170	175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
 180 185 190

Ala Glu Ile Leu Ser Arg Val Asn
 195 200

<210> 733

<211> 1194

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1171)

<223> RXN02802

<400> 733

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agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala
 135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595
 Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His
 150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643
 Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Gly Ser
 170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691
 Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val
 185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739
 Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val
 200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787
 Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly
 215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg 835
 Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg
 230 235 240 245

gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag 883
 Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu
 250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc 931
 Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu
 265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979
 Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly
 280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc
 1027
 Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro
 295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc
 1075
 Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val
 310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga
 1123
 Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly
 330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg
 1171
 Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 345 350 355

taaaaccaag gcgttggtgcc acc
 1194

<210> 734

<211> 357

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 734

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15
 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30
 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45
 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60
 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80
 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95
 Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
 145 150 155 160
 Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
 165 170 175
 Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
 180 185 190
 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
 195 200 205
 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
 210 215 220
 Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
 225 230 235 240
 Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
 245 250 255
 Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
 260 265 270
 Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
 275 280 285
 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
 290 295 300

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
 305 310 315 320
 Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
 325 330 335
 Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
 340 345 350
 Leu Asp Ser Leu Gly
 355

<210> 735
 <211> 497
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (7)..(474)
 <223> FRXA02802

<400> 735
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 Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro
 1 5 10 15
 ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99
 Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
 20 25 30
 tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147
 Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
 35 40 45
 tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195
 Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
 50 55 60
 gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243
 Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
 65 70 75
 cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
 Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
 80 85 90 95
 acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
 Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
 100 105 110
 gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
 Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
 115 120 125
 caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
 Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
 130 135 140

ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484
 Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

gcgttggtgcc acc 497

<210> 736
 <211> 156
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 736
 Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu
 1 5 10 15
 Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr
 20 25 30
 Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser
 35 40 45
 Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val
 50 55 60
 Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg
 65 70 75 80
 Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr
 85 90 95
 Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala
 100 105 110
 Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln
 115 120 125
 Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu
 130 135 140
 Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

<210> 737
 <211> 535
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> FRXA00438

<400> 737
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 agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

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atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
      10                      15                      20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
      25                      30                      35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
Gly Leu Gly Ser Pro Ala Leu Tyr Leu Ala Gly Ala Gly Val Gly
      40                      45                      50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
      55                      60                      65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
      70                      75                      80                      85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
      90                      95                      100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
      105                      110                      115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
      120                      125                      130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
      135                      140                      145

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<210> 738

<211> 145

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 738

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Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
  1                      5                      10                      15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
  20                      25                      30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
  35                      40                      45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
  50                      55                      60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
  65                      70                      75                      80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
      85                      90                      95

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Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro
 145

<210> 739
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> RXN00437

<400> 739
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 ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115
 Met Asn Thr Asp Pro
 1 5
 gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr
 10 15 20
 acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys
 25 30 35
 aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp
 40 45 50
 cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro
 55 60 65
 acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys
 70 75 80 85
 cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys
 90 95 100
 atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala
 105 110 115
 gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp
 135 140 145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579
 Val Gly Leu
 150

<210> 740

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
 1 5 10 15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
 20 25 30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 35 40 45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140

Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

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ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20                      25                      30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35                      40                      45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50                      55                      60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65                      70                      75                      80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85                      90                      95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100                      105                      110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaaacct cgacatcgcc cgc 383
Gly Ser Thr Asp Trp Val Gly Leu
      115                      120

<210> 742
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 742
Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
  1                      5                      10                      15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20                      25                      30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35                      40                      45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50                      55                      60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65                      70                      75                      80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85                      90                      95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100                      105                      110

Gly Ser Thr Asp Trp Val Gly Leu
      115                      120

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<210> 743
<211> 591
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(568)  
<223> RXN00439
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tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc 115																
Met Ser Glu Leu Thr 5																
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163																
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys 20																
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211																
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg 35																
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259																
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp 50																
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307																
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr 65																
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355																
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr 85																
gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg 403																
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val 100																
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg 451																
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val 115																
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag 499																
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys 130																
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa 547																
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys 145																
tct ggg gat tgg tct gtt cag tgacagctct ggttatcggt gcg 591																
Ser Gly Asp Trp Ser Val Gln 155																

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<210> 744
<211> 156
<212> PRT
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<213> Corynebacterium glutamicum

<400> 744

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Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1              5              10              15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
      20              25              30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
      35              40              45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50              55              60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
 65              70              75              80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg
      85              90              95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu
      100             105             110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile
      115             120             125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
      130             135             140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
145              150              155

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<210> 745

<211> 218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

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act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act   48
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1              5              10              15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg   96
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
      20              25              30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc   144
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
      35              40              45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt   192
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50              55              60

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cag tgacagctct gggtatcggt gcg

218

Gln

65

<210> 746

<211> 65

<212> PRT

<213> Corynebacterium glutamicum

<400> 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
 20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
 35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50 55 60

Gln

65

<210> 747

<211> 358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> FRXA00442

<400> 747

ctgccaccgc agactgtctg atcaggatcc cggcgcgggac tacggtggag gaaaacgaca 60

togttaagat ttaccatttc aactaacagg agttaattta atg agc gag ctc acc 115
 Met Ser Glu Leu Thr
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
 40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
 55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85

gtg
 Val

358

<210> 748
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 748
 Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
 65 70 75 80

Leu Gly Lys Ile Thr Val
 85

<210> 749
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(559)
 <223> RXA00440

<400> 749
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tgtcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg_aca gct ctg gtt 115
 Val Thr Ala Leu Val
 1 5

atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163
 Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser
 10 15 20

ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro
 25 30 35

gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr
 55 60 65
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu
 70 75 80 85
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val
 90 95 100
 ccg acc gca gta ttg tgc cgc acc gtc gcg ggc acc atc ggc ggc agt 451
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser
 105 110 115
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr
 120 125 130
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly
 135 140 145
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582
 His His Glu His
 150

<210> 750

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130 135 140

Gly Thr Leu Gln Gly His His Glu His
145 150

<210> 751
<211> 1287
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1264)
<223> RXN00441

<400> 751
agccttgagg gcggtgatta tgcttttggc tgtctatgtc ctcattcattg gagccatcgg 60
agcggttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115
Met Ser Arg Ser Pro
1 5
gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163
Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser
10 15 20
acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala
25 30 35
gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp
40 45 50
ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val
55 60 65
ggg cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg
70 75 80 85
ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro
90 95 100
aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn
105 110 115
ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe
120 125 130
ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro
135 140 145
gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				
1027				
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				
1075				
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				
1123				
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				
1171				
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				
1219				
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				
1264				

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385

taagatttac ccattcaact aac
 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15

Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
 260 265 270
 Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
 275 280 285
 Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
 290 295 300
 Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
 305 310 315 320
 Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
 325 330 335
 Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
 340 345 350
 Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
 355 360 365
 His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
 370 375 380
 Lys Arg His Arg
 385

<210> 753

<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(792)

<223> FRXA00441

<400> 753

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Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp	
1 5 10 15	
att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg	96
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser	
20 25 30	
gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc	144
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val	
35 40 45	
gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca	192
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser	
50 55 60	
gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt	240
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu	
65 70 75 80	
cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac	288
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His	

85										90					95					
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336																			
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																				
100 105 110																				
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																			
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																				
115 120 125																				
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																			
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																				
130 135 140																				
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480																			
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																				
145 150 155 160																				
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528																			
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																				
165 170 175																				
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576																			
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																				
180 185 190																				
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																			
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																				
195 200 205																				
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																			
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																				
210 215 220																				
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																			
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																				
225 230 235 240																				
ggt tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac	768																			
Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																				
245 250 255																				
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																			
Tyr Gly Gly Gly Lys Arg His Arg																				
260																				

<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

Ile	Pro	Ala	Thr	Pro	Gln	Gly	Gln	Phe	Ile	Arg	Leu	Gln	Gly	Ser	Asp
1				5					10					15	

Ile	Thr	Ala	Gly	Asp	Glu	Ile	Ile	Pro	Ala	Gly	Thr	Glu	Leu	Asn	Ser
			20					25					30		

Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val
		35					40					45			

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
 50 55 60
 Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80
 Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
 85 90 95
 Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
 100 105 110
 Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125
 Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140
 Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160
 Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
 165 170 175
 Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190
 Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205
 Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220
 Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
 225 230 235 240
 Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
 245 250 255
 Tyr Gly Gly Gly Lys Arg His Arg
 260

<210> 755

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575

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 580 585 590

Leu Leu Pro Ala Thr Arg Arg Arg
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 <223> FRXA02086

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 Met Ser Leu Arg Phe
 1 5
 gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
 10 15 20
 tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
 25 30 35
 gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
 40 45 50
 tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
 55 60 65
 cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
 70 75 80 85
 ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
 90 95 100
 tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
 105 110 115
 gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
 120 125 130
 gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
 135 140 145
 aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600

Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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aac

603

<210> 760

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 760

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Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
 35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
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Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
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Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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<210> 761

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1303)

<223> RXN02648

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 Met Ser Gln Asn Arg

1															5		
atc	agg	acc	act	cac	gtt	ggc	tcc	ttg	ccc	cgt	acc	cca	gag	cta	ctt	163	
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu		
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gat	gca	aac	atc	aag	cgt	tct	aac	ggc	gag	att	ggg	gag	gag	gaa	ttc	211	
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe		
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ttc	cag	att	ctg	cag	tct	tct	gta	gat	gac	gtg	atc	aag	cgc	cag	gtt	259	
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val		
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gac	ctg	ggc	atc	gac	atc	ctt	aac	gag	ggc	gaa	tac	ggc	cac	gtc	acc	307	
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr		
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tcc	ggc	gca	gtt	gac	ttc	ggc	gca	tgg	tgg	aac	tac	tcc	ttc	acc	cgc	355	
Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg		
70						75						80				85	
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403	
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
90						95						100					
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
105						110						115					
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
120						125						130					
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
135						140						145					
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
150						155						160				165	
ctg	aag	aag	ggc	atg	aac	gca	gca	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
170						175						180					
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
185						190						195					
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gca	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
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tac	aag	atc	atc	acc	gat	gca	ggc	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
215						220						225					
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
230						235						240				245	

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt
 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
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 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

aacgaggggtt gct
 1326

<210> 762

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
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 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

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 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(525)
 <223> FRXA02648

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 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
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<210> 764

<211> 175

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 764

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 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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<210> 765

<211> 784

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

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Met Ser Gln Asn Arg
1 5
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
200 205 210
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

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Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
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<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 767

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                                         1           5

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Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
                        10                15                20

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Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
                        25                30                35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
                        40                45                50

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Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
                        55                60                65

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Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
                        70                75                80                85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
                        90                95                100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
                        105                110                115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
                        120                125                130

agttttgtcc atc 513

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<210> 768

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 768

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
  1           5           10           15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
      20                25                30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
      35                40                45

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Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 769
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA01515

<400> 769
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ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tgc gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
 275 280

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 771

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agcgcgtctc cacaattaag cagtggctac attaggtggt atg agt tct ttg ccg 115
Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggg ggc aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc 211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val
25 30 35

att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly
40 45 50

ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca 307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro
55 60 65

atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt 355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val
70 75 80 85

gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca 403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala
90 95 100

acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag 451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln
105 110 115

gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg 499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly
120 125 130

gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg 547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val
135 140 145

gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt 595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg
150 155 160 165

gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc 643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe
170 175 180

ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag 691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu
185 190 195

gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat 739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp
200 205 210

ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc 787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly
215 220 225

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acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
 250

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
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Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

245

250

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<210> 773
<211> 684
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(661)  
<223> RXA01719
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 170 175 180

acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684
 Thr Leu Pro Lys Ala His
 185

<210> 774
 <211> 187
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 774
 Met Asn Ile Ile Ile Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly
 1 5 10 15
 Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
 20 25 30
 Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
 35 40 45
 Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60
 Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80
 His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95
 Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110
 Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125
 Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140
 Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
 145 150 155 160
 Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
 165 170 175
 Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
 180 185

<210> 775
 <211> 1332
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(1309)
 <223> RXA01720

<400> 775

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ctatatattt gagtgtttat tgtcgaaaaa ggggtttcaa gtg gca cag caa cgc 115
                               Val Ala Gln Gln Arg
                               1                               5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
                               10                               15                               20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
                               25                               30                               35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
                               40                               45                               50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
                               55                               60                               65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
70                               75                               80                               85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
                               90                               95                               100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
                               105                               110                               115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
                               120                               125                               130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
135                               140                               145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
150                               155                               160                               165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
                               170                               175                               180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
185                               190                               195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
200                               205                               210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

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215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
	250	255	260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
	265	270	275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
	280	285	290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
	295	300	305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
310	315	320	325
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
	330	335	340
gcg ctg aag gcg cgg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
	345	350	355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
	360	365	370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
	375	380	385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
390	395	400	
taaatagaata tcatcattct tgc			
1332			

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Val Ala Gln Gln Arg Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp
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 Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His
 20 25 30
 Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
 35 40 45
 Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
 50 55 60
 Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
 65 70 75 80
 Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
 85 90 95
 Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
 100 105 110
 Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
 115 120 125
 Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
 130 135 140
 Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
 145 150 155 160
 Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
 165 170 175
 Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
 180 185 190
 Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro
 195 200 205
 Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His
 210 215 220
 Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys
 225 230 235 240
 Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala
 245 250 255
 Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe
 260 265 270
 Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly
 275 280 285
 Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala
 290 295 300
 Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu
 305 310 315 320

Gly Arg Met

gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 385
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg
 1105
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc
 1153
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
 1201
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgtcagggtcc
 1237
 Gly Arg

<210> 778
 <211> 402
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 778
 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15

Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
 115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
 130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
 145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
 165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp


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<210> 779
<211> 1229
<212> DNA
<213> Corynebacterium glutamicum
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<400> 779
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Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
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qcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96

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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
			20					25					30				
gcg	att	gat	ggt	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
		35					40					45					
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
	50					55					60						
gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
65					70				75						80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggt	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
			85					90						95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
			100					105					110				
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
		115					120					125					
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val		
	130					135					140						
tta	ggc	cct	gcc	caa	att	ggt	ttg	ctc	gca	gct	gtt	ggt	cgc	tcc	aaa	480	
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
145					150					155					160		
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
				165					170					175			
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180					185					190				
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggt	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195				200						205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggt	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210					215					220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225					230					235					240		
gct	gtt	ggc	ggt	gct	ggt	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245					250					255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggt	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			
1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
	325	330	335
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
	340	345	350
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
	355	360	365
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
	370	375	380
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
	385	390	395
ggt cga tagttcgatg cgtaatgcac cgt			
1229			
Gly Arg			

<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys
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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30		

Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
		35					40					45			

Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
65					70					75					80
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105					110		
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145						150					155				160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225						230					235				240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
	290					295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305						310					315				320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340				345						350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
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Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

Gly Arg

<210> 781

<211> 708

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (685)

<223> RXA02629

<400> 781

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atctgcatct aatcaagtag ccaagtatga gtgaggaaca atg agc aag gat cca 115
Met Ser Lys Asp Pro
1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Glu
55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
135 140 145
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tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val
 185 190 195

tgagttgggtc ggggtgtgagt aga 708

<210> 782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg
 1 5 10 15

Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190

Ser Val Val
 195

<210> 783
 <211> 402
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(379)
 <223> RXA02318

<400> 783
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 cagtaagcgc atgtgcgcca ttttaaggca agatggggcc atg aat tcg ctt ttc 115
 Met Asn Ser Leu Phe
 1 5
 gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163
 Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His
 10 15 20
 ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211
 Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile
 25 30 35
 gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259
 Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr
 40 45 50
 tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307
 Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile
 55 60 65
 acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355
 Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys
 70 75 80 85
 acc ttg gcc att tcg gca gag gct taagggttaa gattatgagc aac 402
 Thr Leu Ala Ile Ser Ala Glu Ala
 90

<210> 784
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 784
 Met Asn Ser Leu Phe Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala
 1 5 10 15
 Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys
 20 25 30
 Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro
 35 40 45
 Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His
 50 55 60
 Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile



65	70	75	80
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala			
85	90		
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60			
gttccaggaa	atccatggct	gctggaagga	gcaacgccta
		atg	cat
		Met	His
		1	
			gca
			ggt
			ttg
			Leu
			5
115			
tcc	atc	ggg	tcc
aaac	atg	gat	gat
cgcg	tac	gcg	ctg
ctc	aac	aca	gtg
163			
Ser	Ile	Gly	Ser
Asn	Met	Asp	Asp
Arg	Tyr	Ala	Leu
15			
			Leu
			20
20			
atc	gag	gaa	ttc
aaa	gat	gag	atc
gtg	gcg	cag	tct
gcg	atc	tac	tca
211			
Ile	Glu	Glu	Phe
Lys	Asp	Glu	Ile
30			
			Ala
			Gln
			Ser
			Ala
			Ile
			Tyr
			Ser
			35
35			
acc	cca	ccg	tgg
ggc	att	gag	gat
cag	gat	gaa	ttc
ctc	aac	gca	gtg
259			
Thr	Pro	Pro	Trp
Gly	Ile	Glu	Asp
45			
			Gln
			Asp
			Glu
			Phe
			Leu
			Asn
			Ala
			Val
			50
50			
ctc	ggt	ggt	gag
ggt	gaa	gaa	acc
ccc	atc	gag	ttg
ctg	cgc	cgt	ggc
307			
Leu	Val	Val	Glu
Val	Glu	Glu	Thr
60			
			Pro
			Ile
			Glu
			Leu
			Arg
			Arg
			Gly
			55
55			
caa	aaa	ctc	gaa
gaa	gcc	gcc	gag
cgg	gtc	cgc	gtc
cgc	aaa	tgg	ggg
355			
Gln	Lys	Leu	Glu
Glu	Ala	Glu	Arg
80			
			Val
			Arg
			Lys
			Trp
			Gly
			85
85			
cca	cgc	acc	ctc
gat	gtg	gat	atc
gtg	cag	atc	att
aaa	gat	ggg	gaa
403			
Pro	Arg	Thr	Leu
Asp	Val	Asp	Ile
90			
			Val
			Gln
			Ile
			Lys
			Asp
			Gly
			100
100			
gag	atc	ctt	tct
gag	gat	ccc	gaa
ctg	acc	ttg	cca
cac	cct	tgg	gct
451			
Glu	Ile	Leu	Ser
Glu	Asp	Pro	Glu
110			

150

155

gca

600

<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala
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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01304

<400> 787

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 Met Pro Ala Gln Asn
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

	10	15	20	
gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag	211			
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
25 30 35				
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt	259			
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
40 45 50				
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc	307			
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
55 60 65				
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg	355			
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
70 75 80 85				
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg	403			
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
90 95 100				
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta	451			
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
105 110 115				
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc	499			
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
120 125 130				
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg	547			
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
135 140 145				
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt	596			
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
150 155 160				
ttgcttatcg acg	609			

<210> 788

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 788

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Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala	
20 25 30	
Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val	
35 40 45	
Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu	
50 55 60	
Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly	
65 70 75 80	

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<210> 789
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1258)
<223> RXS02556
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<400> 789																
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							Leu	Ile	Val	Ser	Thr					
							1				5					
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val	
				10					15					20		
atc	aaa	gca	acg	ctt	cct	ctc	gtg	ggc	ggc	aag	att	aat	gag	atc	acg	211
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr	
				25					30					35		
ccg	gtt	ttc	tac	aac	aag	atg	ttt	gcg	gct	cac	cca	gaa	ttg	atc	gct	259
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala	
				40					45					50		
aac	acc	ttc	aac	cgt	ggc	aat	cag	aag	caa	ggc	gat	cag	cag	aag	gcg	307
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala	
		55					60					65				
ctg	gcg	gct	tcg	att	gca	acg	ttt	gcc	acc	atg	ctc	ggt	act	cct	gat	355
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp	
		70					75					80				85
gct	cct	gac	cca	gtt	cag	ctg	ctg	tcc	cgc	att	ggc	cac	aag	cac	gtg	403
Ala	Pro	Asp	Pro	Val	Gln	Leu	Leu	Ser	Arg	Ile	Gly	His	Lys	His	Val	
				90					95					100		

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
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ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
120 125 130	
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
150 155 160 165	
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
170 175 180	
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
200 205 210	
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
230 235 240 245	
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
250 255 260	
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
280 285 290	
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	
1027	
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
295 300 305	
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1075	
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu	
310 315 320 325	
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1123	
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile	

330

335

340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag
1171

Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta
1219

Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca
1268

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375 380 385

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1281

<210> 790

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 790

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Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335
 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350
 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
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 Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
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 Ile Ser
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 <213> Corynebacterium glutamicum

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 <222> (101)..(967)
 <223> RXS02560

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 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro

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Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro			
			25					30					35					
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259		
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val			
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cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307		
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile			
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att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355		
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile			
	70				75					80					85			
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403		
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly			
				90				95						100				
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451		
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu			
			105					110					115					
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499		
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu			
		120					125					130						
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg	547		
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly			
	135					140					145							
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595		
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu			
	150				155					160					165			
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggg	tcg	gtg	cgc	aac	gat	gcg	643		
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala			
				170				175					180					
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691		
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val			
			185				190						195					
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att	739		
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile			
		200				205					210							
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787		
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr			
	215				220						225							
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835		
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr			
	230				235					240					245			
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883		
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala			
			250					255						260				

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
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attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
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Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225		230		235		240									
Arg	Ala	Leu	Asp	Thr	Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp
				245					250					255	
Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr
			260					265					270		
Asn	Arg	Gln	Phe	Leu	Arg	Gly	Val	Phe	Glu	Arg	Ala	Gly	Phe	Gly	Leu
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Arg

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 <211> 1425
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1402)
 <223> RXA00382

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 ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115
 Met Thr Ser Ser Asn
 1 5
 acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163
 Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro
 10 15 20
 ggt ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211
 Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln
 25 30 35
 gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259
 Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp
 40 45 50
 gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307
 Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met
 55 60 65
 ggt cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg 355
 Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val
 70 75 80 85
 gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc 403
 Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala
 90 95 100
 caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451
 Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn
 105 110 115
 tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac 499

Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg Leu Ala Arg Gly Tyr	
120	125 130
act cag cgt tcc aag att ttg aag ttt gag ggc tgc tac cac ggc cac	547
Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly Cys Tyr His Gly His	
135	140 145
gtc gat gcg ctg ctc gca tct gct ggt tct ggt gtc gca act ttc gct	595
Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly Val Ala Thr Phe Ala	
150	155 160 165
ctg cct gat tcc cca ggc atc acc ggc gct cag act tct gac act att	643
Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln Thr Ser Asp Thr Ile	
	170 175 180
gtt gtt cct tac aac gac att gaa gcc gtg cgc aac gct ttt gcg gag	691
Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg Asn Ala Phe Ala Glu	
	185 190 195
tac cca ggc gag atc gcc tgc atc atc gca gag gca gcc ggt ggc aac	739
Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu Ala Ala Gly Gly Asn	
	200 205 210
atg ggc acc gtc gct cca aag gac aac ttt aac gac aag ctt ctc gcg	787
Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn Asp Lys Leu Leu Ala	
	215 220 225
atc gct cac gct gac ggc gcg ctg ctg atc ctc gat gaa gtc atg acc	835
Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu Asp Glu Val Met Thr	
230	235 240 245
ggc ttc cgc acc tct tac cgt ggc tgg ttc ggc gta gac aag gtt gcc	883
Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly Val Asp Lys Val Ala	
	250 255 260
gct gac ctg gtc acc ttc ggc aag gtc gtc tcc ggc ggc cta cct gcc	931
Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser Gly Gly Leu Pro Ala	
	265 270 275
gca gcg ttt ggc ggc aag gct gaa atc atg aac atg ctg gcc cca cag	979
Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn Met Leu Ala Pro Gln	
	280 285 290
ggc ccc gtc tac caa gca ggc aca ctg tcc ggc aac ccg gtt gcg gtc	
1027	
Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Val Ala Val	
	295 300 305
gca gct ggt cgg gca tcg ctt aag ctt gcc gac gaa tcc ctc tac aca	
1075	
Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp Glu Ser Leu Tyr Thr	
310	315 320 325
acc atc aac gcc aac gca gat cgt ctc cac ggt ttg atc tct gat gcc	
1123	
Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly Leu Ile Ser Asp Ala	
	330 335 340
tta acc cac gaa ggc gta gcc cac cac att cag cgt gcc tca aac atg	
1171	
Leu Thr His Glu Gly Val Ala His His Ile Gln Arg Ala Ser Asn Met	

345 350 355
 ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg
 1219
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met
 360 365 370
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg
 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg
 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc
 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac
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 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser
 425 430
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 1425

<210> 794

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 794

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 35 40 45
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
 340 345 350
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
 355 360 365
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
 385 390 395 400
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 405 410 415
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys
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 Ala Ser



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<212> DNA
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<222> (101)..(1210)
<223> RXA00156
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Met Asn Glu Arg Thr 5																
tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163																
Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu 20																
ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211																
Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg 35																
ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259																
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His 50																
ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307																
Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala 65																
aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355																
Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr 85																
ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403																
Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln 100																
atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451																
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala 115																
tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499																
Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly 130																
atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547																
Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys 145																
ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa 595																
Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln 165																
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Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu 180																

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
 Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
 185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
 200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
 215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
 250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
 265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
 280 285 290

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 1027
 Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
 295 300 305

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 1075
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 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
 330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg
 1171
 Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
 345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat
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<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 796

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Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
      35              40              45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
      50              55              60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
      65              70              75              80

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
      85              90              95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
      100              105              110

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
      115              120              125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
      130              135              140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
      145              150              155              160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
      165              170              175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
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Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
      195              200              205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
      210              215              220

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
      225              230              235              240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
      245              250              255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
      260              265              270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
      275              280              285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
      290              295              300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
      305              310              315              320

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Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
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Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys
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His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
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Ala Asn
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<223> RXA00624

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 Met Ser Gly Arg Leu
 1 5

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
 Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
 25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
 Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
 40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
 Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
 105 110 115

tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499
 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe

120	125	130	
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Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
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Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
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Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu			
	35	40	45
Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg			
	50	55	60
Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg			
	65	70	75
Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu			
	85	90	95
Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile			
	100	105	110
Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu			
	115	120	125
Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn			
	130	135	140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
 145 150 155 160
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
 165 170 175
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
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 Ala Ala Gln Leu Ala
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 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
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 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

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Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
	165	170	175
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
	180	185	190
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
	195	200	205
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	210	215	220
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	225	230	235
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
	245	250	255
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
	260	265	270
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
	275	280	285
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
	290	295	300
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Pro Ala Asp Leu Leu Asp Ser			
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Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr															
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Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu															
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Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys															
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Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu															
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Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg															
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Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg															
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Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser															
				245					250					255																
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			260					265					270																	
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		275					280					285																		
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu															
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 <223> RXA00884

<400> 801

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Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
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Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
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Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
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Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
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Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
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Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
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Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
                        135                      140                      145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
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                        170                      175                      180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
                        185                      190                      195

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 215 220 225
 gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
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 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
 265 270 275
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 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
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 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
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 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
 330 335 340
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 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
 345 350 355
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 1219
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
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<212> PRT

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<400> 802

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 35 40 45
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
 50 55 60
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
 65 70 75 80
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
 85 90 95
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
 100 105 110
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
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 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
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325 330 335
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 Met Thr Leu Lys Ile 5
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 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg 20
 10 15
 gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr 35
 25 30
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 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly 50
 40 45
 gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp 65
 55 60
 gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg 85
 70 75 80
 ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile 100
 90 95
 gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
 Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly 115
 105 110
 ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
 Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro 130
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522

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<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

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 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala
 115 120 125

Gln Gly Asn Pro Pro
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<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(535)

<223> FRXA02503

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 Met Thr Leu Lys Ile
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

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<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

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 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His
 145

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 <222> (101)..(1222)
 <223> RXA00377

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 Val Trp Leu Leu Phe
 1 5
 cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr
 10 15 20
 att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala
 25 30 35
 gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln
 40 45 50
 gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser
 55 60 65
 atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu
 70 75 80 85
 cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp
 90 95 100
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 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala
 105 110 115
 ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val
 120 125 130
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 Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly
 135 140 145

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 Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
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 Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
 170 175 180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct 691
 Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
 185 190 195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat 739
 Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
 200 205 210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt 787
 Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
 215 220 225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
 Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
 230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
 Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
 250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
 Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
 265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg 979
 Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
 280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
 1027
 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
 295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
 1075
 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
 310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
 1123
 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
 330 335 340

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 1171
 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
 345 350 355

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 1219
 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
 360 365 370

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 1245
 Ser

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 <213> Corynebacterium glutamicum

<400> 808
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 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
 35 40 45
 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
 50 55 60
 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
 65 70 75 80
 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
 85 90 95
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
 100 105 110
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
 115 120 125
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
 130 135 140
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
 145 150 155 160
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
 165 170 175
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
 180 185 190
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
 195 200 205
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
 210 215 220
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
 225 230 235 240
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
 245 250 255
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260										265					270															
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Trp	Arg	Val	Pro	Leu	Asp	Lys	Ala	Ala	Glu	Arg	Ile	Ala	Ala	Val	Ser															
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Gln	Thr	Ala	Val	Asp	Ala	Gly	His	Ala	Thr	Gly	His	Ile	Phe	Asn	Leu															
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(658)

<223> RXN02504

<400> 809

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                               Val Gly Thr Ser Ala
                               1                               5

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att 163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
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ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
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ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
                               55                               60                               65

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
70                               75                               80                               85

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 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

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 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
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<210> 810

<211> 186

<212> PRT

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<400> 810

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 20 25 30

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 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
 145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
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<212> DNA

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 Met Leu Val Met Leu
 1 5

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 Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu
 10 15 20

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 Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu
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gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259
 Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn
 40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307
 Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr
 55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355
 Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His
 70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403
 Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly
 90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451
 Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly
 105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499
 Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu
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561

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 <212> PRT
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 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu
 115 120 125

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Arg Ser
 145

<210> 813
 <211> 1449
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1426)
 <223> RXN01162

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 Met Tyr Ile Val Gly
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Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val		
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Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro		
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ctc	gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355	
Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile		
	70				75					80					85		
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Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu		
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Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp		
		120					125					130					
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547	
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met		
	135					140					145						
gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595	
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys		
	150				155					160					165		
gcc	cgc	ttg	ggc	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643	
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly		
				170					175					180			
caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691	
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln		
			185					190					195				
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Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr		
		200					205					210					
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gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835	
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His		
	230				235					240					245		
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883	
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg		

250										255					260					
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac	931																			
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp																				
265 270 275																				
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg	979																			
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met																				
280 285 290																				
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta																				
1027																				
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu																				
295 300 305																				
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt																				
1075																				
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val																				
310 315 320 325																				
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt																				
1123																				
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser																				
330 335 340																				
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta																				
1171																				
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val																				
345 350 355																				
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc																				
1219																				
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly																				
360 365 370																				
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct																				
1267																				
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro																				
375 380 385																				
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag																				
1315																				
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys																				
390 395 400 405																				
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc																				
1363																				
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg																				
410 415 420																				
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act																				
1411																				
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr																				
425 430 435																				
cca gaa gcg gtg aat tagcatcaaa aaccaacccc atg																				
1449																				
Pro Glu Ala Val Asn																				
440																				

<210> 814
 <211> 442
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 814

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
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Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175

Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190

Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205

Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220

Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240

Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255

Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270

Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285

Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu

290	295	300	
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser			
305	310	315	320
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly			
	325	330	335
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys			
	340	345	350
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile			
	355	360	365
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp			
	370	375	380
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu			
	385	390	395
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile			
	405	410	415
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val			
	420	425	430
Thr Lys Pro Val Thr Pro Glu Ala Val Asn			
	435	440	
<210> 815			
<211> 1345			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1345)			
<223> FRXA01162			
<400> 815			
catcgaatac gtgccctgct gaatagatga catcgacagag atctataaga gtcagtgggtt 60			
gtcgggggttt cacagtcact tattctatgc aggatccacc atg tat atc gtg ggg 115			
		Met Tyr Ile Val Gly	
		1 5	
att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163			
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp			
	10	15	20
tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211			
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val			
	25	30	35
gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259			
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro			
	40	45	50
gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307			
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly			

55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att			355
Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile			
70	75	80	85
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag			403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu			
	90	95	100
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg			451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu			
	105	110	115
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat			499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp			
	120	125	130
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg			547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met			
	135	140	145
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tgc ctt gct tgc			595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys			
	150	155	160
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga			643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly			
	170	175	180
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa			691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln			
	185	190	195
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg			739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr			
	200	205	210
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc			787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
	215	220	225
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
	230	235	240
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
	250	255	260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
	265	270	275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
	280	285	290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			
1027			
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295 300 305
 cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt
 1075
 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val
 310 315 320 325
 gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt
 1123
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser
 330 335 340
 gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta
 1171
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val
 345 350 355
 caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc
 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370
 cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct
 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385
 gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag
 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
 390 395 400 405
 ctt cac aca ctc caa gaa caa cac ggc gga
 1345
 Leu His Thr Leu Gln Glu Gln His Gly Gly
 410 415

 <210> 816
 <211> 415
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 816
 Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1 5 10 15
 Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30
 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly
 405 410 415

<210> 817
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXA01692

<400> 817
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 gttcgggttc tggcaattgt tgggactagg attaatgccc atg acg att tcc caa 115
 Met Thr Ile Ser Gln
 1 5
 gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct 163
 Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu Ile Gly Gly Gly Pro
 10 15 20
 ggt gca tgg gac tta att acg gtg cgt ggg atg aat cgc ctt cag gag 211
 Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met Asn Arg Leu Gln Glu
 25 30 35
 gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa 259
 Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro Thr Asp Glu Leu Glu
 40 45 50
 aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt 307
 Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val Asp Val Ser Lys Leu
 55 60 65
 ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt 355
 Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr Asn Glu Met Leu Val
 70 75 80 85
 gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac 403
 Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg Leu Lys Gly Gly Asp
 90 95 100
 cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag 451
 Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu Glu Phe Leu Gly Glu
 105 110 115
 cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc 499
 His Gly Ile Glu Cys Glu Val Ile Pro Gly Val Thr Ser Ala Val Ser
 120 125 130
 gtt cca gcg gcg gca ggt att cct att act aat cgg gga gtg gtg cat 547
 Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn Arg Gly Val Val His
 135 140 145
 tcc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca 595
 Ser Phe Thr Val Val Ser Gly His Leu Pro Pro Gly His Pro Lys Ser
 150 155 160 165
 ctg gtt gat tgg gct gcg ttg gcc aaa tcg ggt ggc acc ttg tcc atc 643
 Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly Gly Thr Leu Ser Ile
 170 175 180

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
 Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp
 185 190 195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr
 200 205 210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
 215 220 225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
 Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly
 230 235 240 245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
 Gln Val Ala Gly Leu
 250

<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 818

Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu
 1 5 10 15

Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met
 20 25 30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
 35 40 45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
 50 55 60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
 65 70 75 80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
 85 90 95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
 100 105 110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val
 115 120 125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn
 130 135 140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
 145 150 155 160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
 165 170 175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala
 180 185 190
 Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val
 195 200 205
 Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu
 210 215 220
 Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala
 225 230 235 240
 Val Tyr Val Ile Gly Gln Val Ala Gly Leu
 245 250

<210> 819
 <211> 1917
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1894)
 <223> RXN00371

<400> 819
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 acgttggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
 Met Thr Ile Ala His
 1 5
 aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20
 gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35
 tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50
 ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65
 aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85
 gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100
 cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
 Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
 120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
 Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
 135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
 Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
 150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
 Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
 170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
 Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
 185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
 Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile
 200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
 Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
 215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
 Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
 230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
 Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn
 250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
 Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
 265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
 Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
 280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat
 1027
 Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp
 295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg
 1075
 Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp
 310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca
 1123
 Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala
 330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct
 1171

Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser
 345 350 355
 gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc
 1219
 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly
 360 365 370
 atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca
 1267
 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala
 375 380 385
 gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt
 1315
 Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg
 390 395 400 405
 tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct
 1363
 Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala
 410 415 420
 gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc
 1411
 Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr
 425 430 435
 agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa
 1459
 Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu
 440 445 450
 gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca
 1507
 Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala
 455 460 465
 acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa
 1555
 Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu
 470 475 480 485
 gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat
 1603
 Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp
 490 495 500
 atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc
 1651
 Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr
 505 510 515
 tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac
 1699
 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His
 520 525 530
 cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct
 1747
 Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala

535 540 545
 gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta
 1795
 Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
 550 555 560 565

 cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct
 1843
 Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
 570 575 580

 aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg
 1891
 Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala
 585 590 595

 tct taaaaggttt ttactaggg tgt
 1917
 Ser

 <210> 820
 <211> 598
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 820
 Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
 1 5 10 15

 Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30

 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45

 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110

 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125

 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495

[illegible]

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<210> 821
<211> 1024
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (1024)  
<223> FRXA00371
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<400> 821															
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acgttggctcg ttttcgagac aagtactaga aaagatat															115
Met Thr Ile Ala His															
1 5															
aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc															163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser															
10 15 20															
gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt															211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val															
25 30 35															
tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca															259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro															
40 45 50															
ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt															307
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu															
55 60 65															
aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act															355
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr															
70 75 80 85															
gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att															403
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile															

90										95					100					
cct	gtg	ccg	gaa	gat	aag	ctt	cag	gct	gcg	gaa	gat	gag	tac	gag	cgc	451				
Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg					
			105					110					115							
atc	tgc	att	gaa	gcg	aag	gag	aac	ggc	gca	cgc	cgt	aag	cct	cct	cgt	499				
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg					
		120					125					130								
cca	gca	cca	cca	acc	gct	gca	gag	atc	acg	gaa	gtt	tct	gag	gcg	act	547				
Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr					
	135					140					145									
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggc	gga	595				
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly					
150					155					160					165					
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643				
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr					
			170						175					180						
ctg	gct	gag	atc	tct	gca	gtt	tcc	gag	gct	ggc	ctg	gag	ttc	cag	gtg	691				
Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val					
			185					190					195							
gtt	cca	ggc	atg	tct	ttg	cct	gca	acg	gtt	cct	gca	ttt	gcg	gga	att	739				
Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile					
		200					205					210								
gcg	ttg	ggc	tct	acc	tac	acc	gaa	act	gat	gtc	aac	ggc	caa	aac	ttg	787				
Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu					
	215					220					225									
gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835				
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala					
230					235				240						245					
cgc	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cgc	aat	883				
Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn					
				250					255					260						
atg	tct	ttg	gaa	act	cct	gtt	tct	gtc	acc	gct	aac	ggc	acc	acc	cgt	931				
Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg					
			265					270					275							
ttg	cag	cgc	acc	tat	gac	acc	act	tta	ggc	ctg	ttg	cac	aag	ctt	gat	979				
Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp					
		280					285					290								
gct	gaa	cta	agc	gga	cct	ttg	gtt	gtt	acc	ttg	ggc	aag	ggc	gtg						
1024																				
Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	Gly	Lys	Gly	Val						
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<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
 1 5 10 15
 Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
 305

<210> 823
 <211> 755
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(732)
 <223> FRXA00374

<400> 823
 acc att tct gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc 48
 Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15
 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggttt ttactaggg tgt 755
 Arg Lys Ala Ser

<210> 824

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 824

Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15

Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

Arg Lys Ala Ser

<210> 825
 <211> 1467
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1444)
 <223> RXN00383

<400> 825
 ccatatctttt aaccttggtc atggtgtgct tcctaatacgt gtggcggaag atattactga 60

agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115
 Met Arg Phe Ala Ile
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser 150 155 160 165			595
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu 170 175 180			643
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu 185 190 195			691
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys 200 205 210			739
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala 215 220 225			787
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu 230 235 240 245			835
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile 250 255 260			883
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala 265 270 275			931
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala 280 285 290			979
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc 1027 Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser 295 300 305			
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc 1075 Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe 310 315 320 325			
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg 1123 Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala 330 335 340			
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc 1171 Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg 345 350 355			
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc 1219 Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360 365 370
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg
 1267
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val
 375 380 385
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct
 1315
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala
 390 395 400 405
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa
 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca
 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat
 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445
 tga
 1467

<210> 826

<211> 448

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 826

Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
 1 5 10 15
 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 435 440 445



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<210> 827
<211> 382
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(382)
<223> FRXA00376
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[illegible]

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<210> 828
<211> 94
<212> PRT
<213> Corynebacterium glutamicum
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<400> 828
Met  Arg  Phe  Ala  Ile  Ile  Gly  Ala  Gly  Leu  Ala  Gly  Leu  Thr  Ala  Ala
  1          5          10          15

Tyr  Glu  Ile  His  Lys  Ala  Asp  Pro  Thr  Ala  Gln  Ile  Asp  Val  Leu  Glu
      20          25          30

Ala  Gly  Glu  Arg  Ile  Gly  Gly  Lys  Leu  Phe  Thr  Val  Pro  Phe  Ala  Ser
      35          40          45

Gly  Pro  Thr  Asp  Ile  Gly  Ala  Glu  Ala  Phe  Leu  Ala  Ala  Arg  Ser  Asp

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50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
 85 90

<210> 829
 <211> 1037
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1014)
 <223> FRXA00383

<400> 829
 gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att 48
 Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
 1 5 10 15

 tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat 96
 Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

 act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat 144
 Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45

 gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat 192
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60

 cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag 240
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80

 gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc 288
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95

 ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg 336
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110

 ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc 384
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125

 gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa 432
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140

 ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct 480
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160

 gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca 528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg
 1008
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 ctg gga taagcaccca aaaacactat tga
 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 Leu Gly

<210> 831
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXA01253

<400> 831
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 gagacctcaa aaaggctctg gagaaagggga ccgaacaata atg acc acc ctc aac 115
 Met Thr Thr Leu Asn
 1 5
 atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc 163
 Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly
 10 15 20
 aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct 211
 Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala
 25 30 35
 gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat 259
 Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp
 40 45 50
 ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc 307
 Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr
 55 60 65
 gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc 355
 Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly
 70 75 80 85
 cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc 403
 Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser
 90 95 100
 ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc 451
 Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala
 105 110 115
 acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca 499
 Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr
 120 125 130
 cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc 547
 Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly
 135 140 145
 ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca 595
 Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro
 150 155 160 165
 ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc 643
 Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala
 170 175 180

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val
 185 190 195

caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg
 200 205 210

aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala
 215 220 225

ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg
 230 235 240 245

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873
 Ala Glu Arg Leu Ala
 250

<210> 832

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr
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Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190
 Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205
 Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220
 Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240
 Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833

<211> 1044

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1021)

<223> RXA02134

<400> 833

tgatgaacga catgtcgaca ttttcttccg ccggcgctcga tggaccacctta aacgcctctt 60

ccgaagcgcc cgagcaaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115
 Met Ser Gly Lys Ala 5
 1

ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn 20
 10 15

ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu 35
 25 30

ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val 50
 40 45

atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala 65
 55 60

atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp 85
 70 75 80

gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn 100
 90 95

cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly 115
 105 110

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tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
      120                      125                      130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
      135                      140                      145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
      150                      155                      160                      165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
      170                      175                      180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
      185                      190                      195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
      200                      205                      210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
      215                      220                      225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
      230                      235                      240                      245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
      250                      255                      260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
      265                      270                      275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
      280                      285                      290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
1021
Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
      295                      300                      305

taaagcgggtg gcgtcttttg gga
1044

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<210> 834

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 834

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Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
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Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
 275 280 285
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
 290 295 300
 Ala Met Val
 305

<210> 835
 <211> 1197

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

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aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
                                         Met Val Pro Ala Glu
                                         1           5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
                        10                        15                        20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
                        25                        30                        35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg 259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro
                        40                        45                        50

cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac 307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His
                        55                        60                        65

ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg 355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu
                        70                        75                        80                        85

cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att 403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile
                        90                        95                        100

gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac 451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp
                        105                        110                        115

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc 499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile
                        120                        125                        130

gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag 547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys
                        135                        140                        145

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att 595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile
                        150                        155                        160                        165

tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc 643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala
                        170                        175                        180

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc 691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg

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	185		190		195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc						739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile						
	200		205		210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc						787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala						
	215		220		225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc						835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe						
	230		235		240	245
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt						883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val						
		250		255		260
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc						931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala						
		265		270		275
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc						979
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser						
	280		285		290	
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg						
1027						
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met						
	295		300		305	
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag						
1075						
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys						
	310		315		320	325
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc						
1123						
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly						
		330		335		340
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg						
1171						
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr						
		345		350		355
gag taactttcta agcgatgtcc ggc						
1197						
Glu						

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys

1

5

10

15

Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340

345

350

Pro Glu Gln Asn Thr Glu
355

<210> 837

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA02136

<400> 837

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ccctcgtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

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 ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga 642
 Gly Leu Pro Leu Glu Leu Lys Thr Phe
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agg 645

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 <213> Corynebacterium glutamicum

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 Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
 35 40 45
 Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
 50 55 60
 Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp
 65 70 75 80
 Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
 85 90 95
 Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
 100 105 110
 Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
 115 120 125
 Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
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 Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
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cgc	cgc	gag	ttg	acg	gtg	ggg	ttg	gat	gct	ggg	gac	ggg	ccg	att	tta	96	
Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
agg	cag	agc	ttt	gat	gtt	ggg	ttt	ttg	ctt	gtc	gac	gcc	tcc	ttc	cac	144	
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		
		35					40					45					
att	cat	atc	aat	ggc	gtg	tct	act	ggg	cag	tcg	gtt	gcg	ccg	gat	gat	192	
Ile	His	Ile	Asn	Gly	Val	Ser	Thr	Gly	Gln	Ser	Val	Ala	Pro	Asp	Asp		
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gta	gtt	gag	gtg	gtg	cgt	ggg	ttg	gct	gat	gct	tcg	gag	ttg	tcc	gtg	240	
Val	Val	Glu	Val	Val	Arg	Gly	Leu	Ala	Asp	Ala	Ser	Glu	Leu	Ser	Val		
		65			70					75					80		
gaa	agt	gtt	gct	gag	ttg	tgt	act	ccc	gtg	gca	ccg	gtt	tca	tta	tct	288	
Glu	Ser	Val	Ala	Glu	Leu	Cys	Thr	Pro	Val	Ala	Pro	Val	Ser	Leu	Ser		
				85				90						95			
gag	gca	cag	ggg	aat	cct	gcg	cct	att	ggg	tgg	ttg	gag	cat	gat	ggc	336	
Glu	Ala	Gln	Gly	Asn	Pro	Ala	Pro	Ile	Gly	Trp	Leu	Glu	His	Asp	Gly		
			100					105					110				
gtg	gtg	tcg	ttg	ggg	gcg	ggg	att	cca	ggg	ggg	cgg	gtg	gag	gct	cgt	384	
Val	Val	Ser	Leu	Gly	Ala	Gly	Ile	Pro	Gly	Gly	Arg	Val	Glu	Ala	Arg		
		115				120						125					
tta	gcg	cgt	ttt	att	gcg	gtg	att	gag	gcg	gag	acc	act	att	acc	cca	432	
Leu	Ala	Arg	Phe	Ile	Ala	Val	Ile	Glu	Ala	Glu	Thr	Thr	Ile	Thr	Pro		
		130				135					140						
tgg	aat	tcg	ttg	atc	att	cat	gat	ttg	tat	gag	ggg	gtt	gca	gaa	cag	480	
Trp	Asn	Ser	Leu	Ile	Ile	His	Asp	Leu	Tyr	Glu	Gly	Val	Ala	Glu	Gln		
				150				155						160			
gtg	gtg	aag	gtt	ctg	gct	ccc	atg	ggg	ttg	gtt	ttt	gat	gct	aat	tca	528	
Val	Val	Lys	Val	Leu	Ala	Pro	Met	Gly	Leu	Val	Phe	Asp	Ala	Asn	Ser		
				165				170						175			
ccg	ctt	ctg	gag	tca	ccg	gct	ttg	taactcgcca	ttggtgcacg	tct						575	
Pro	Leu	Leu	Glu	Ser	Pro	Ala	Leu										
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<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

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Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		

35 40 45
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
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 Pro Leu Leu Glu Ser Pro Ala Leu
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1177)
 <223> RXN01810

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 gcttcaccgt cggcaaccg actggaaaat aaggcttcac atg aat aac gct ttt 115
 Met Asn Asn Ala Phe
 1 5
 cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
 Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
 10 15 20
 gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
 Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
 25 30 35
 att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
 Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
 40 45 50
 aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
 Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc			355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly			
70	75	80	85
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc			403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu			
	90	95	100
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat			451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn			
	105	110	115
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att			499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile			
	120	125	130
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt			547
Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu			
	135	140	145
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc			595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg			
	150	155	160
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg			643
Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met			
	170	175	180
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc			691
Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile			
	185	190	195
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt			739
Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg			
	200	205	210
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc			787
Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr			
	215	220	225
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt			835
Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly			
	230	235	240
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att			883
Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile			
	250	255	260
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat			931
Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp			
	265	270	275
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc			979
Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val			
	280	285	290
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt			
1027			
Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295 300 305
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa
 1075
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln
 310 315 320 325
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa
 1123
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln
 330 335 340
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc
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 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly
 345 350 355
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 1200
 Gly Glu

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<400> 842
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 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
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 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr
 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu
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Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
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Leu Tyr Val Gln Gly Gly Glu
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<211> 963

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXS03205

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ggt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu	
260 265 270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn	
275 280 285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg	912



Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963
 Pro Ala Asp Leu Leu Asp Ser
 305 310

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 <213> Corynebacterium glutamicum

<400> 844
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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
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Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255



Ile	Val	Ala	Gly 260	Leu	Asn	Pro	His	Gly 265	Leu	Pro	Phe	Glu	Glu	Ile	Leu
Glu	Met	Tyr	Ala 275	Met	Ala	Gln	Gly 280	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
Gly	Ala	Ile	Ala	Ala	Leu	Val 295	Asp	Leu	Ile	Arg	His 300	Gly	Leu	Val	Leu
Pro 305	Ala	Asp	Leu	Leu	Asp 310	Ser									

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<212> DNA
<213> Corynebacterium glutamicum
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Val	Arg	Gly	Arg	Thr	Phe	Asp	Arg	Ile	Ile	Ala	Asn	Pro	Pro	Phe	Val	
			20					25					30			
gtg	gga	cca	ccg	gaa	att	ggg	cat	gtg	tac	cgc	gat	tcc	ggc	atg	gat	144
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp	
		35					40					45				
cta	gac	ggc	gcg	acc	gcg	ttg	gtg	gtc	aaa	gaa	gcc	tgc	gcg	cat	ctc	192
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu	
	50					55				60						
aac	cct	ggt	ggc	acc	gct	cac	ctg	ctc	ggc	gca	tgg	gtg	cat	tcc	gcg	240
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala	
65				70						75					80	
gat	caa	tcg	tgg	cag	cag	cgc	gtt	gca	gaa	tgg	ttg	ccg	gat	aac	ggt	288
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly	
				85					90					95		
tat	gtt	gct	tgg	gtt	att	gag	cgc	gac	gcc	gtg	agc	ccc	gcg	cag	tat	336
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr	
			100					105					110			
gtg	ggc	acg	tgg	ctt	agt	gat	gag	tcc	ctc	gat	ctg	cgt	agc	ccc	gag	384
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu	
		115					120					125				
gca	gca	gca	cgc	acc	acc	gcg	tgg	ctt	aac	cac	ttt	gaa	aaa	gcc	aag	432
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys	
	130					135					140					

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 gag gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 846

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50	55	60
Asn Pro Gly Gly Thr	Ala His Leu Leu Gly	Ala Trp Val His Ser Ala
65	70	75 80
Asp Gln Ser Trp Gln	Gln Arg Val Ala Glu Trp	Leu Pro Asp Asn Gly
	85	90 95
Tyr Val Ala Trp Val	Ile Glu Arg Asp Ala Val	Ser Pro Ala Gln Tyr
	100	105 110
Val Gly Thr Trp Leu	Ser Asp Glu Ser Leu Asp	Leu Arg Ser Pro Glu
	115	120 125
Ala Ala Ala Arg Thr	Thr Ala Trp Leu Asn His	Phe Glu Lys Ala Lys
	130	135 140
Val Gln Gly Val Gly	Phe Gly Phe Ile Ala Ile	Gln Arg Leu Glu Glu
145	150	155 160
Asp Glu Ala Asp Glu	Lys Ser Asp Ile Leu Ala	Glu Ser Met Thr Gln
	165	170 175
Tyr Phe Glu Asp Pro	Leu Gly Pro Glu Ile Glu	Glu Tyr Phe Thr Arg
	180	185 190
Thr Ala Trp Leu Arg	Glu Gln Thr Arg Asp Ser	Ile Leu Ser Ser Arg
	195	200 205
Phe Lys Val Arg Pro	Gly Val Ala Arg Glu Gln	Ile Ser Leu Ala Asp
	210	215 220
Ala Glu Glu Gly Met	Gly Phe Ser Pro Val Thr	Leu Arg Leu Thr Arg
225	230	235 240
Thr Asp Gly Pro Arg	Trp Ser His Asp Val Asp	Glu His Val Ala Ser
	245	250 255
Ile Val Ala Gly Leu	Asn Pro His Gly Leu Pro	Phe Glu Glu Ile Leu
	260	265 270
Glu Met Tyr Ala Met	Ala Gln Gly Ile Glu Gly	Glu Ser Leu His Asn
	275	280 285
Gly Ala Ile Ala Ala	Leu Val Asp Leu Ile Arg	His Gly Leu Val Leu
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Pro Ala Asp Leu Leu	Asp Ser	
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<210> 847

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXC01715

<400> 847

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                                   Val Ser Glu Leu Asp
                                   1                               5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
                                   10                               15                               20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
Arg Ala Ile Pro Gly Ala Leu Asp Asp Arg Thr Glu Val Thr Asp
                                   25                               30                               35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
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gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
                                   55                               60                               65

atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
                                   70                               75                               80                               85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
                                   90                               95                               100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
                                   105                               110                               115

ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
                                   120                               125                               130

tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
                                   135                               140                               145

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
                                   150                               155                               160                               165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
                                   170                               175                               180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
                                   185                               190                               195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
                                   200                               205                               210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

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215 220 225 819

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Val Leu Pro
230

<210> 848
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 848
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Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
35 40 45
Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
50 55 60
Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
65 70 75 80
Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
85 90 95
Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
100 105 110
Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
115 120 125
Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
130 135 140
Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
145 150 155 160
Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
165 170 175
Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
180 185 190
Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
195 200 205
His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
210 215 220
Ala Asp Leu Ile Lys Val Leu Pro
225 230

<210> 849
<211> 1587

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00420

<400> 849

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				Met	Asn	Ser	Ser	His	
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ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggc	gcc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro	
				10					15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggc	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25					30					35			

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	
	55					60					65					

ggc	gtg	att	gcc	cgt	ggc	atg	ggc	cgt	tcc	tat	ggc	gac	cca	gcc	caa	355
Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr	Gly	Asp	Pro	Ala	Gln	
70					75					80					85	

aac	gcc	ggc	ggc	ctt	gtc	att	gac	atg	cag	cca	ctg	aac	aaa	atc	cac	403
Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro	Leu	Asn	Lys	Ile	His	
				90					95					100		

tcg	att	gat	cct	gat	tct	gcg	atc	gtc	gat	gta	gat	ggc	ggc	gtc	acc	451
Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val	Asp	Gly	Gly	Val	Thr	
			105					110						115		

ctc	gat	cag	ctc	atg	aag	gct	gcc	ctg	cca	tat	ggc	ctc	tgg	gtt	cct	499
Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr	Gly	Leu	Trp	Val	Pro	
		120					125					130				

gtc	ctt	ccc	ggc	acc	cgc	caa	gtc	acc	atc	ggc	ggc	gca	atc	gga	cca	547
Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly	Gly	Ala	Ile	Gly	Pro	
	135					140						145				

gac	atc	cac	ggc	aag	aac	cac	cac	tct	gca	ggc	tcc	ttc	ggc	gac	cac	595
Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly	Ser	Phe	Gly	Asp	His	
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gtg	gtc	tcc	atg	gaa	ctc	ctc	gtt	gca	gac	gga	cgc	atc	ctg	cac	ctc	643
Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	His	Leu	
				170					175					180		

gag	cca	gaa	ggc	acc	gcc	gaa	gac	cca	cag	ggc	gac	ctg	ttc	tgg	gca	691
Glu	Pro	Glu	Gly	Thr	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Leu	Phe	Trp	Ala	

185	190	195	
acc gtt ggt ggc atg ggc ctg	acc ggc atc atc gtc	cgt gca cgc atc	739
Thr Val Gly Gly Met Gly Leu	Thr Gly Ile Ile Val	Arg Ala Arg Ile	
200	205	210	
cgc atg acc aag acg gaa acc gcc	tac ttc att gcg gac acc gac cgc		787
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg			
215	220	225	
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag			835
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu			
230	235	240	245
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag			883
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu			
	250	255	260
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt			931
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu			
	265	270	275
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag			979
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys			
	280	285	290
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1027			
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp			
	295	300	305
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc			
1075			
Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala			
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1123			
Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr			
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caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag			
1171			
Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys			
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ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct			
1219			
Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro			
	360	365	370
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca			
1267			
Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala			
	375	380	385
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc			
1315			
Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser			
	390	395	400
			405

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1363

Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
410 415 420

ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc
1411

Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac
1459

Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat
1507

Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt
1555

Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
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1587

Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

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20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450
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 Met Ser Arg Arg Leu Glu Leu Ser
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 <212> DNA
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 <222> (1)..(540)
 <223> FRXA00420

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 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
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 Leu Glu Leu Ser
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 <213> Corynebacterium glutamicum

<400> 852
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 35 40 45
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
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 Leu Glu Leu Ser
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(622)
 <223> FRXA00426



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Met Asn Ser Ser His																5
1																
ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc	163															
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro																
10 15 20																
cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc																211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr																
25 30 35																
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Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val																
40 45 50																
cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc																307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg																
55 60 65																
ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa																355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln																
70 75 80 85																
aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac																403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His																
90 95 100																
tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc																451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr																
105 110 115																
ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct																499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro																
120 125 130																
gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca																547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro																
135 140 145																
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Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His																
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gtg gtc tcc atg gaa ctc ctc gtt gca																622
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170																

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<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 854

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
1 5 10 15



His	Gly	Ala	Leu	Pro	Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg		
			20				25						30				
Thr	Ala	Pro	Thr	Thr	Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile		
			35				40						45				
Ile	Val	Asp	Ala	Val	Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro		
			50				55						60				
Asp	Tyr	Leu	Lys	Arg	Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr		
			65				70						75	80			
Gly	Asp	Pro	Ala	Gln	Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro		
			85						90						95		
Leu	Asn	Lys	Ile	His	Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val		
			100						105						110		
Asp	Gly	Gly	Val	Thr	Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr		
			115						120						125		
Gly	Leu	Trp	Val	Pro	Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly		
			130						135						140		
Gly	Ala	Ile	Gly	Pro	Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly		
			145						150						155	160	
Ser	Phe	Gly	Asp	His	Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala				
			165						170								

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<210> 855
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(907)  
<223> RXN00708
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taccgatccc ctccctgaa gtttcgctaa cctggcgctac atg act ctt tcc ctt 115
               Met Thr Leu Ser Leu
               1         5

cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt 163
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val
               10               15               20

gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc 211
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr
               25               30               35

gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag 259
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu
               40               45               50

tcg ggt gtc ccc cgc qaq qaa ttg att gtt acc aqt aag ctc cct gcc 307

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Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	
55						60					65					
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	
70					75					80					85	
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	
				90					95					100		
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	
			105					110					115			
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu	
			120				125						130			
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggg	gaa	ctg	ccg	gcc	547
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	
			135			140					145					
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	
150					155					160					165	
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	
				170					175					180		
agc	aac	ggg	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	
			185					190					195			
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His	
			200				205					210				
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	
			215			220					225					
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	
230					235					240					245	
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	
				250					255					260		
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtta	catcaagggtt	ccg						930
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe									
				265												

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

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Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
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Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
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Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
          35          40          45
Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
          50          55          60
Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
          65          70          75          80
Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
          85          90          95
Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
          100          105          110
Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
          115          120          125
Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
          130          135          140
Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
          145          150          155          160
Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
          165          170          175
Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
          180          185          190
Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
          195          200          205
Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
          210          215          220
Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
          225          230          235          240
Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
          245          250          255
Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
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<210> 857

<211> 695

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(672)

<223> FRXA00708

<400> 857

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Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
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att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga      96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
                               20                               25                               30

cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc      144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
                               35                               40                               45

gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc      192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
   50                               55                               60

gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag      240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
   65                               70                               75                               80

cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc      288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
                               85                               90                               95

cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc      336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
                               100                               105                               110

tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc      384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
                               115                               120                               125

att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa      432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
   130                               135                               140

gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc      480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
   145                               150                               155                               160

gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca      528
Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
                               165                               170                               175

cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag      576
Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
                               180                               185                               190

att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc      624
Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
   195                               200                               205

aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc      672
Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
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tagatagtta catcaagggtt ccg      695

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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
 35 40 45
 Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
 50 55 60
 Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
 65 70 75 80
 His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
 85 90 95
 Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
 100 105 110
 Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125
 Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
 130 135 140
 Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
 145 150 155 160
 Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175
 Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190
 Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205
 Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220

<210> 859
 <211> 1038
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1015)

<223> RXA02373

<400> 859

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                Met Ser Val Val Gly
                1                    5

acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
                10                    15                    20

caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
                25                    30                    35

cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
                40                    45                    50

ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
                55                    60                    65

gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
                70                    75                    80                    85

aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
                90                    95                    100

gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
                105                    110                    115

gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
                120                    125                    130

gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
                135                    140                    145

gtt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
                150                    155                    160                    165

atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
                170                    175                    180

gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
                185                    190                    195

ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
                200                    205                    210

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gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala
 215 220 225

gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835
 Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala
 230 235 240 245

cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro
 250 255 260

aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp
 265 270 275

ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
 280 285 290

aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag
 1025
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn
 295 300 305

gtaaggccct gca
 1038

<210> 860

<211> 305

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 860

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Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile
 35 40 45

Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
 50 55 60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
 65 70 75 80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
 85 90 95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
 100 105 110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
 115 120 125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
 130 135 140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
 145 150 155 160
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
 165 170 175
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
 180 185 190
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
 195 200 205
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
 210 215 220
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
 225 230 235 240
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
 245 250 255
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
 260 265 270
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
 275 280 285
 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
 290 295 300
 Asn
 305

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 <211> 1683
 <212> DNA
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 <223> RXS00389

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 Met Ile Thr Ala Thr
 1 5
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
 10 15 20
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
 25 30 35
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259

Pro	Ser	Tyr	Ser	Leu	Ala	Asn	Ser	Ala	Gln	Leu	Arg	Ala	Ala	Thr	Thr		
		40					45					50					
tcg	gcg	aag	cga	gct	ttt	gaa	agc	tac	cga	ctc	act	act	cca	gag	gtt	307	
Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val		
		55				60					65						
aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355	
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser		
		70			75					80					85		
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggc	ttg	gga	act	acc	403	
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr		
				90					95					100			
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451	
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe		
			105					110					115				
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499	
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
		120				125						130					
gga	cgc	cgg	att	gat	ctt	cgc	cag	cgt	cag	gtt	ccg	ttg	gga	cca	gtc	547	
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
	135					140					145						
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggc	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
	150				155					160					165		
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	gtt	ttt	aag	643	
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
				170					175					180			
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggc	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
		200					205					210					
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
	215					220					225						
aat	atc	acg	gca	atc	ggc	ttt	acc	ggc	tca	cgc	cag	ggc	ggc	ttg	gca	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
	230				235					240				245			
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
				250					255					260			
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265				270					275					
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
505 510 515

ata gac cgt taatagctgg tctttacatt tgc
1683

Ile Asp Arg
520

<210> 862

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

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20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
 500 505 510
 Ala Val Pro Arg Glu Ile Asp Arg
 515 520

<210> 863
 <211> 882
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(859)
 <223> RXS00419

<400> 863
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 Met Leu Asn Ala Val
 1 5
 ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163
 Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
 10 15 20
 att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc 211
 Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
 25 30 35
 ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag 259
 Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
 40 45 50
 atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg 307
 Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala
 55 60 65
 ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac 355
 Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn
 70 75 80 85
 ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403
 Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn
 90 95 100
 gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg 451
 Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val
 105 110 115
 aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499
 Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe
 120 125 130
 gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc 547
 Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly
 135 140 145
 cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt 595
 Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly
 150 155 160 165
 ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt 643
 Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
 170 175 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
 230 235 240 245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
 Ala Ile Phe Arg Lys Leu Pro Phe
 250

<210> 864
 <211> 253
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 864
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Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
 20 25 30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
 180 185 190
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
 195 200 205
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
 210 215 220
 Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
 225 230 235 240
 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 245 250

<210> 865

<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXC00416

<400> 865

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att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac	96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp	
20 25 30	
cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc	144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly	
35 40 45	
ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga	192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly	
50 55 60	
tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt	240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly	
65 70 75 80	
tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct	288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala	
85 90 95	
tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg	336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val	
100 105 110	
gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat	384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn	
115 120 125	
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	

130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc			480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala			
145	150	155	160
ggc ggc att att tac ttg ggt gtt tgc gct act ttc tat act ttg ttc			528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe			
	165	170	175
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg			576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala			
	180	185	190
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg			624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu			
	195	200	205
ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt			672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu			
	210	215	220
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac			720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His			
225	230	235	240
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca			768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser			
	245	250	255
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg			816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val			
	260	265	270
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg			864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val			
	275	280	285
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac			912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn			
	290	295	300
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc			960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala			
305	310	315	320
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat			1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr			
	325	330	335
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc			1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr			
	340	345	350
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa			1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln			
	355	360	365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat
 1152
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca
 1200
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag
 1248
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac
 1296
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg
 1344
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc
 1392
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg
 1440
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc
 1488
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg
 1536
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
 500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg
 1584
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg
 1632
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa
 1673
 Val Val Thr His Asn Glu
 545 550

<210> 866
 <211> 550
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 866

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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
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Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
              35              40              45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50              55              60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65              70              75              80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
              85              90              95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
              100              105              110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
              115              120              125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
              130              135              140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
              145              150              155              160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
              165              170              175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
              180              185              190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
              195              200              205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
              210              215              220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
              225              230              235              240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
              245              250              255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
              260              265              270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
              275              280              285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
  
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290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
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Val Val Thr His Asn Glu 545 550		

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<211> 1059

<212> DNA

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<220>

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<222> (101)..(1036)

<223> RXC02206

<400> 867

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                                         Met Val Gly Ser Ser
                                         1                               5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                               10                               15                               20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
                               25                               30                               35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
                               40                               45                               50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
                               55                               60                               65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
                               70                               75                               80                               85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                               90                               95                               100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
                               105                               110                               115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
                               120                               125                               130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
                               135                               140                               145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
                               150                               155                               160                               165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                               170                               175                               180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
                               185                               190                               195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
                               200                               205                               210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

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215	220	225	
gga cgc gac gca gaa gtc	caa agc tac cta gat	aat cga ggc cgc atc	835
Gly Arg Asp Ala Glu Val	Gln Ser Tyr Leu Asp	Asn Arg Gly Arg Ile	
230	235	240	245
att gtc gat gct ctt gat	act gca gcc aaa gga	tta ggc att agc ccc	883
Ile Val Asp Ala Leu Asp	Thr Ala Ala Lys Gly	Leu Gly Ile Ser Pro	
250	255	260	
gct gtc aca gcc acc acc	tggtgtg cgt gat cgt	ccc gga gtg aca gct	931
Ala Val Thr Ala Thr Thr	Trp Val Arg Asp Arg	Pro Gly Val Thr Ala	
265	270	275	
gtc atc gtg ggc gct cgc	aca cat gaa cag ctg	tca cat ctt ctc aag	979
Val Ile Val Gly Ala Arg	Thr His Glu Gln Leu	Ser His Leu Leu Lys	
280	285	290	
gcg gaa tcg gtg act ttg	cca aca cca atc aca	caa gcc ctt gat gat	
1027			
Ala Glu Ser Val Thr Leu	Pro Thr Pro Ile Thr	Gln Ala Leu Asp Asp	
295	300	305	
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1059			
Val Ser Leu			
310			
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<400> 868			
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20	25	30	
Lys Ala Phe Ile Asn Ser	Gly Gly Thr Leu Ile	Asp Val Ser Pro Asn	
35	40	45	
Tyr Thr Thr Gly Val Ala	Glu Glu Met Leu Gly	Thr Met Leu Asp Ala	
50	55	60	
Glu Val Ser Arg Ser Ala	Val Val Ile Ser Ser	Ser Ala Gly Val Asn	
65	70	75	80
Pro Ala Leu Pro Leu Gly	Arg Arg Val Asp Cys	Ser Arg Arg Asn Leu	
85	90	95	
Ile Ala Gln Leu Asp Val	Thr Leu Arg Ala Leu	Asn Thr Asp Tyr Leu	
100	105	110	
Asp Leu Trp Ser Val Gly	Tyr Trp Asp Glu Gly	Thr Pro Pro His Glu	
115	120	125	
Val Ala Asp Thr Leu Asp	Tyr Ala Val Arg Thr	Gly Arg Val Arg Tyr	
130	135	140	

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXS03074

<400> 869
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 870

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 870

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 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr



100	105	110	
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr			
115	120	125	
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe			
130	135	140	
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr			
145	150	155	160
Glu Ala Pro Ile Lys Gln			
165			
<210> 871			
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<212> DNA			
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<220>			
<221> CDS			
<222> (101) .. (598)			
<223> FRXA02906			
<400> 871			
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115			
Met Thr Gln Ser Ala			
1 5			
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163			
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn			
10 15 20			
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211			
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu			
25 30 35			
ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259			
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu			
40 45 50			
ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307			
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile			
55 60 65			
gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355			
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala			
70 75 80 85			
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403			
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala			
90 95 100			
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451			
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala			
105 110 115			
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499			

Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 872
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 872
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160
 Glu Ala Pro Ile Lys Gln
 165

<210> 873
 <211> 1752
 <212> DNA
 <213> Corynebacterium glutamicum

1204

Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly	
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Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr	
215	220 225
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc	835
Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val	
230	235 240 245
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg	883
Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val	
	250 255 260
gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat	931
Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp	
	265 270 275
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat	979
Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp	
	280 285 290
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc	
1027	
Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly	
	295 300 305
acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt	
1075	
Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu	
310	315 320 325
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc	
1123	
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe	
	330 335 340
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc	
1171	
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly	
	345 350 355
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg	
1219	
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu	
	360 365 370
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc	
1267	
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val	
	375 380 385
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct	
1315	
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala	
390	395 400 405
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc	
1363	
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala	

410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 874
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 874
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 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe



370					375					380					
Ser 385	Pro	Arg	Gly	Val	Ala 390	Gly	Ile	Asp	Gly	Ser 395	Val	Ala	Gln	Ala	Ile 400
Gly	Thr	Ser	Leu	Ala 405	Val	Gln	Ser	Arg	His 410	Pro	Asp	Glu	Ile	Arg 415	Ala
Pro	Arg	Thr	Val 420	Ala	Leu	Leu	Gly	Asp 425	Leu	Ser	Phe	Leu	His 430	Asp	Ile
Gly	Gly	Leu 435	Leu	Ile	Gly	Pro	Asp 440	Glu	Pro	Arg	Pro	Glu 445	Asn	Leu	Thr
Ile 450	Val	Val	Ser	Asn	Asp 455	Asn	Gly	Gly	Gly	Ile	Phe 460	Glu	Leu	Leu	Glu
Thr 465	Gly	Ala	Asp	Gly	Leu 470	Arg	Pro	Asn	Phe	Glu 475	Arg	Ala	Phe	Gly	Thr 480
Pro	His	Asp	Ala	Ser 485	Ile	Ala	Asp	Leu	Cys 490	Ala	Gly	Tyr	Gly	Ile 495	Glu
His	Gln	Val 500	Val	Asp	Asn	Leu	Gln	Asp 505	Leu	Ile	Ile	Ala	Leu 510	Val	Asp
Thr	Thr	Glu 515	Val	Ser	Gly	Phe	Thr 520	Ile	Ile	Glu	Ala	Ser 525	Thr	Val	Arg
Asp 530	Thr	Arg	Arg	Ala	Gln 535	Gln	Gln	Ala	Leu	Met	Asp 540	Thr	Val	His	

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<210> 875
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1057)  
<223> RXA02319
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agaccttggc catttcggca gaggcctaag gttaaagatt .atg agc aac tac agc      115
                                         Met Ser Asn Tyr Ser
                                           1                      5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt      163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
                        10                          15                20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc      211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
                        25                          30                35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat      259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
                    40              45              50
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gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac	307
Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His	
55 60 65	
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc	355
Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly	
70 75 80 85	
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa	403
Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln	
90 95 100	
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc	451
Arg Ile Arg Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg	
105 110 115	
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa	499
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys	
120 125 130	
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc	547
Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg	
135 140 145	
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc	595
Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly	
150 155 160 165	
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc	643
Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg	
170 175 180	
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac	691
Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp	
185 190 195	
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac	739
Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn	
200 205 210	
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg	787
Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met	
215 220 225	
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa	835
Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu	
230 235 240 245	
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc	883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr	
250 255 260	
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc	931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu	
265 270 275	
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg	979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met	
280 285 290	

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
 1027
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
 295 300 305
 ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
 1077
 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 310 315
 aaa
 1080

<210> 876
 <211> 319
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 876
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 20 25 30
 Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45
 Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60
 Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80
 Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95
 Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110
 Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125
 Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140
 Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160
 Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175
 Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190
 Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205
 Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
 290 295 300
 Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 305 310 315

<210> 877
 <211> 1017
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXS00393

<400> 877
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 aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
 265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
 280 285 290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

<210> 879

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA00393

<400> 879

tctatttcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga	tcgagtatgt	gatggggaaa	gatagagggt	atg	tct	cac	acg	gaa	115
				Met	Ser	His	Thr	Glu	
				1				5	

ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
			10					15						20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25					30					35			

gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
		40				45						50				

ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggg	gtg	aat	tac	gcc	aat	gat	307
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp	
	55					60					65					

tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggg	cct	ctg	355
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu	
70					75					80					85	

cga	ctc	act	ggg	tct	ggg	ttg	gct	gag	ccg	aag	aaa	gtg	aaa	gct	gcg	403
Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala	
			90						95					100		

gcg	ttt	att	tct	ttc	ggg	atc	gca	ggg	gtc	gcc	ggc	acc	gcg	ctg	agc	451
Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser	
			105					110					115			

ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg	499
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu	
		120				125						130				

ggc	gcg	tgg	ttc	tac	acc	ggc	ggg	aaa	aat	cct	tat	ggg	tac	cgc	ggg	547
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly	
	135					140					145					

ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg	595
Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	Leu	Val	Ala	Val	Met	
150					155					160					165	

gga	acg	cag	ttc	acc	caa	acc	ggg	tcc	gtc	agc	tgg	gcc	ggg	ttg	gcc	643
Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala	
				170					175					180		

gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn	
			185					190					195			

```

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
      200                      205                      210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
      215                      220                      225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
      230                      235                      240                      245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
      250                      255                      260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
      265                      270                      275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
      280                      285                      290

```

```

cat tagcgtttag ctaaaacgct ttt
1005
His

```

```

<210> 880
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

```

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<400> 880
Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
  1                      5                      10                      15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
      20                      25                      30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
      35                      40                      45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
      50                      55                      60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
      65                      70                      75                      80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
      85                      90                      95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
      100                      105                      110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
      115                      120                      125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

```

130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly 145 150 155 160		
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser 165 170 175		
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly 180 185 190		
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr 195 200 205		
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys 210 215 220		
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu 225 230 235 240		
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu 245 250 255		
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp 260 265 270		
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro 275 280 285		
Cys Ser Arg Ala Trp His 290		

<210> 881
 <211> 843
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(820)
 <223> RXA00391

<400> 881
 atcttgtaga tcccaccgca attctgggag atctcgagga cgcaatctct ggaagaaaac 60
 tttcctcccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct 115
 Leu Leu Arg Asp Ser
 1 5
 caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163
 Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala
 10 15 20
 act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211
 Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu
 25 30 35
 aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259
 Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu
 40 45 50

```

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
    55                60                65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
    70                75                80                85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
                90                95                100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
                105                110                115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
                120                125                130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
                135                140                145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
                150                155                160                165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
                170                175                180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
                185                190                195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
                200                205                210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
                215                220                225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggg ggattgaagt 840
Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
                230                235                240

tgc 843

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<210> 882

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

```

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
  1             5             10             15

```


Ala	Leu	Val	Met	Ala	Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	
			20					25					30			
Gln	Leu	Thr	Pro	Leu	Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	
		35					40					45				
Phe	Leu	Gly	Gly	Glu	Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	
	50					55					60					
Ile	Ala	Gly	Met	Gln	Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	
65					70					75					80	
Pro	Leu	Ala	Ile	Asp	Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	
				85					90					95		
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser	
			100					105					110			
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile	
		115					120					125				
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu	
	130					135					140					
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val	
145					150					155					160	
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly	
				165					170					175		
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu	
			180					185					190			
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His	
		195					200					205				
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu	
	210					215					220					
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His	
225					230					235					240	

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<210> 883
<211> 384
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(361)  
<223> RXS02908
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<400> 883
gccaacgagg gttggtttac cacctctgat tcaggtgaac tccacgacgg gattctcacc 60
.
gtgactggtc gcgtggatac cgcgcattga ttccgggtgga ttg aag ttg cac cca 115
                                Leu Lys Leu His Pro
```

												1					5	
gag	gta	ctg	gaa	cgt	gcc	atc	gca	gat	att	aaa	ggg	gtc	acc	gcg	gcg	163		
Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	Thr	Ala	Ala			
				10					15					20				
tgt	gtt	gtg	ggg	att	ccc	gat	ccc	cga	tta	ggc	caa	gca	att	gtg	gcc	211		
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala			
				25					30					35				
gcg	tac	tcc	gga	tcg	atc	agt	ccg	tct	gaa	gtt	att	gaa	ggc	ctc	gac	259		
Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp			
				40					45					50				
gat	cta	cct	cgt	tgg	cag	ctt	ccc	aaa	cgg	ctg	aag	cat	ctg	gaa	tct	307		
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser			
				55					60					65				
ttg	ccc	agc	att	ggg	cct	gga	aaa	gct	gat	cga	cgt	gct	atc	gcg	aag	355		
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys			
				70					75					80			85	
ctg	ttt	tagtcttcat				tcttgctggc				tgc						384		
Leu	Phe																	

```
<210> 884
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 884
Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
  1                      5                      10                      15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
          20                      25                      30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
          35                      40                      45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
  50                      55                      60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
  65                      70                      75                      80

Arg Ala Ile Ala Lys Leu Phe
          85

```

```
<210> 885
<211> 705
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(682)  
<223> RXA00997
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<400> 885

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cccatctgtg gcagatcgaa tgcacccacc gcggagaagt cgtcgcacga accacactgc 60
gcacccatggt gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1                               5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10                               20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25                               30                               35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40                               45                               50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55                               60                               65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70                               75                               80                               85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90                               95                               100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105                               110                               115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                     120                               125                               130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                     135                               140                               145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                     150                               155                               160                               165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                     170                               175                               180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                     185                               190

atcttgcacc tga 705

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<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

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Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
  1              5              10              15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
          20              25              30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
          35              40              45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
          50              55              60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
          65              70              75              80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
          85              90              95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
          100              105              110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
          115              120              125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
          130              135              140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
          145              150              155              160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
          165              170              175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
          180              185              190

Lys Lys

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<210> 887

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

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aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaaccgata ctggtgggat  gtg gac gcg gcc gac  115
                               Val Asp Ala Ala Asp
                               1              5

```

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggt cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
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Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
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Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
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Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
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Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
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Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
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Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
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Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
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Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
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Asn	Asp	Val	Pro	Asn	Ala	Phe	Val	Thr	Ala	Phe	Asp	Ile	Ser	Ser	Gln
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Met	Leu	Lys	Tyr	Ala	Gly	His	Asp	His	Asn	Val	His	Leu	Val	Gln	Ala
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Asp	Ala	Met	Ser	Leu	Pro	Tyr	Ala	Asp	Ser	Ser	Phe	Asp	Val	Val	Phe
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Ser	Val	Phe	Gly	Ala	Ile	Pro	Phe	Val	Glu	Asp	Ser	Ala	Ala	Leu	Met
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Lys	Glu	Ile	Ala	Arg	Val	Leu	Lys	Pro	Gly	Gly	Arg	Leu	Ile	Phe	Ser
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Ile	Thr	His	Pro	Met	Arg	Trp	Ile	Phe	Leu	Asp	Asp	Pro	Gly	Pro	Ala
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Gly	Leu	Thr	Ala	Ile	Thr	Ser	Tyr	Phe	Asp	Gln	Arg	Gly	Tyr	Val	Glu
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Glu	Asp	Glu	Glu	Thr	Gly	Ala	Leu	Ser	Tyr	Ala	Glu	Gln	His	Arg	Thr
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Met	Gly	Ala	Arg	Ile	Asn	Glu	Leu	Ile	Asp	Ala	Ser	Leu	His	Leu	Asp
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His	Leu	Ile	Glu	Pro	Glu	Trp	Pro	Asp	Glu	Leu	Glu	Glu	Asn	Trp	Gly
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Gln	Trp	Ser	Pro	Leu	Arg	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Ala	Ile	Phe
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Leu	Ala	Thr	Tyr	Arg	Pro
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                               Val Ala Lys Ala Asp
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tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
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aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
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Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
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Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
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Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
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ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
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Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
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Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
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gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
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acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
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cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
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Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp			
35	40	45	
Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val			
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Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp			
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Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys			
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Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala			
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Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp			
180	185	190	
Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser			
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210

215

220

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Val Thr Ser Pro Glu
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tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr
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cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile
25 30 35

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Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala
40 45 50

gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu
55 60 65

cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu
70 75 80 85

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Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly
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Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe
105 110 115

cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr
120 125 130

ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys
135 140 145

cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly

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att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe	230	235	240	245
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Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

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Trp	Tyr	Pro	Lys	Gly	Ile	Asp	Ala	Gly	Thr	Glu	Val	Asp	Ser	Val	Asp	
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Gly	Pro	Ser	Ala	Phe	Val	Glu	Thr	Tyr	Thr	Pro	Glu	Leu	Leu	Arg	Asn	
			180					185					190			
Leu	Pro	Met	Ser	Thr	Thr	Ser	Thr	Gly	His	Asn	Phe	Ala	Glu	Leu	Phe	
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Met Thr Ser Arg Asp 1 5															
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Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg 10 15 20															
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Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly 25 30 35															
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Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg 40 45 50															
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Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly 55 60 65															
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Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn 90 95 100															

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 105 110 115

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 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
 120 125 130

 gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
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 35 40 45

 Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
 50 55 60

 Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala
 65 70 75 80

 Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met
 85 90 95

 Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser
 100 105 110

 Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr
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 Thr Thr Leu Arg Thr Met Val Leu Asn Lys
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Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
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Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
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Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
                        40                        45                        50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
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Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
                        70                        75                        80                        85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
                        90                        95                        100

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Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
                        105                        110                        115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499
Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
                        120                        125                        130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547
Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
                        135                        140                        145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
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Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
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Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
	265	270	275
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Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
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Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu			
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Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg			

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Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser
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Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu
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Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile
				245					250					255	
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser
			260					265					270		
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser
			275					280					285		
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu
			290			295					300				
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu
				310							315				320
Phe	Glu	Gly	Glu	Ala											
				325											

<210> 897

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1447)

<223> RXN00558

<400> 897

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Val Val Lys Lys Pro

1

5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser
 250 255 260

ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca
 1027
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc
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 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa
 1123
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa
 1171
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att
 1219
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc
 1267
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc
 1315
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser
 390 395 400 405

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc
 1363
 Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys
 410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca
 1411
 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala
 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt
 1457
 Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser
 440 445

aggcgatagg ggt
1470

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<210> 898
<211> 449
<212> PRT
<213> Corynebacterium glutamicum
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<400> 898

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Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro
210 215 220

Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile
225 230 235 240

Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile
245 250 255

Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala
260 265 270

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly
 275 280 285
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg
 290 295 300
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val
 305 310 315 320
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile
 325 330 335
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala
 340 345 350
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr
 355 360 365
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu
 370 375 380
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr
 385 390 395 400
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu
 405 410 415
 Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln
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 Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser
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Ser

<210> 899
 <211> 524
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (61)..(501)
 <223> FRXA00558

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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
 1 5 10 15
 ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
 20 25 30
 att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			

<210> 900

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 900

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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
20	25	30	
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
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His Thr Leu
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<210> 901
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1363)
 <223> RXN00626

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 Met Arg Ile Leu Val
 1 5
 atc ggc tgc ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr
 10 15 20
 gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu
 25 30 35
 gga tgc atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu
 40 45 50
 gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile
 55 60 65
 ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala
 70 75 80 85
 gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu
 90 95 100
 ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg
 105 110 115
 act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile
 120 125 130
 gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp
 135 140 145
 ggt ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly 150	Leu	Ser	Ala	Gly	Lys 155	Gly	Val	Val	Val	Thr 160	Pro	Asp	Arg	Ala	Ala 165	
gca	cgt	gct	cac	gta	gat	gca	gtg	ctt	gag	ggc	gga	aat	cca	gtt	ttg	643
Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly	Gly	Asn	Pro	Val	Leu	
				170					175						180	
ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	gtt	tcc	ctg	ttc	tgc	ctg	gtt	691
Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	Phe	Cys	Leu	Val	
			185					190					195			
gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	gat	cac	aag	cgt	739
Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	Asp	His	Lys	Arg	
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gcg	tac	gac	aac	gat	gag	ggc	cca	aac	act	ggg	ggc	atg	ggg	gct	tat	787
Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	Met	Gly	Ala	Tyr	
	215					220					225					
gcg	ccg	ctt	cct	tgg	ctg	cct	gaa	gat	ggc	gtc	cag	cgc	att	gtc	gat	835
Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	Arg	Ile	Val	Asp	
230					235					240					245	
gag	gtc	tgc	gtt	cct	gtt	gct	cgt	gag	atg	gtg	gca	cgt	ggg	tgc	gcg	883
Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	Arg	Gly	Cys	Ala	
				250					255					260		
tac	tcc	ggg	ctg	ctt	tac	gca	ggg	atc	gca	tgg	ggg	gca	gaa	ggc	cct	931
Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	Ala	Glu	Gly	Pro	
			265					270					275			
gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	gaa	acc	cag	gct	979
Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	Glu	Thr	Gln	Ala	
		280					285					290				
gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	ctc	aac	gca	gtt	
1027																
Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	Leu	Asn	Ala	Val	
	295					300					305					
gct	act	gga	acc	ttg	gca	gag	cag	cca	gca	ctg	gag	tgg	gag	gat	gct	
1075																
Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	Trp	Glu	Asp	Ala	
310					315					320				325		
tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	cca	gag	gca	cct	
1123																
Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	Pro	Glu	Ala	Pro	
				330					335					340		
cgt	act	ggg	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	aac	gtt	ctt	cac	
1171																
Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	Asn	Val	Leu	His	
			345				350						355			
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1219																
Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	Ser	Ala	Gly	Gly	
		360					365					370				

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc
 1267
 Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg
 375 380 385
 gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac
 1315
 Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His
 390 395 400 405
 tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc
 1363
 Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile
 410 415 420
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 1386

<210> 902
 <211> 421
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30
 Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
 35 40 45
 Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
 50 55 60
 Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
 65 70 75 80
 Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp
 85 90 95
 Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala
 100 105 110
 Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala
 115 120 125
 Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp
 130 135 140
 Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr
 145 150 155 160
 Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly
 165 170 175
 Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser
 180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
 195 200 205
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
 210 215 220
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
 225 230 235 240
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
 245 250 255
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
 260 265 270
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
 275 280 285
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
 290 295 300
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu
 305 310 315 320
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
 325 330 335
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
 340 345 350
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
 355 360 365
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
 370 375 380
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
 385 390 395 400
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 405 410 415
 Gly Arg Ile Ser Ile
 420

 <210> 903
 <211> 364
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(364)
 <223> FRXA00629

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 aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115
 Met Arg Ile Leu Val



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<222> (1)..(780)  
<223> FRXA00626
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<400> 905

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aat	cca	gtt	ttg	ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	gtt	tcc	ctg	96
Asn	Pro	Val	Leu	Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	
			20					25					30			
ttc	ttc	ctg	gtt	gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	144
Phe	Phe	Leu	Val	Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	
		35					40					45				
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Asp	His	Lys	Arg	Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	
	50					55					60					
atg	ggg	gct	tat	gcg	ccg	ctt	cct	tgg	ctg	cct	gaa	gat	ggc	gtc	cag	240
Met	Gly	Ala	Tyr	Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	
65					70					75					80	
cgc	att	gtc	gat	gag	gtc	tgc	gtt	cct	gtt	gct	cgt	gag	atg	gtg	gca	288
Arg	Ile	Val	Asp	Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	
				85					90					95		
cgt	ggg	tgc	gcg	tac	tcc	ggg	ctg	ctt	tac	gca	ggg	atc	gca	tgg	ggg	336
Arg	Gly	Cys	Ala	Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	
			100					105					110			
gca	gaa	ggc	cct	gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	384
Ala	Glu	Gly	Pro	Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	
		115					120					125				
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Trp	Glu	Asp	Ala	Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	
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Pro	Glu	Ala	Pro	Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	
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Asn	Val	Leu	His	Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	
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Ser	Ala	Gly	Gly	Arg	Val	Leu	Asn	Val	Ile	Gly	Val	Gly	Glu	Thr	Leu	
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gag	gct	gca	cgc	gat	aac	gcg	tac	acc	acc	atc	aag	gac	att	gaa	ctt	720
Glu	Ala	Ala	Arg	Asp	Asn	Ala	Tyr	Thr	Thr	Ile	Lys	Asp	Ile	Glu	Leu	
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 Arg Ile Ser Ile
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 906

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Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln
 35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly
 50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln
 65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala
 85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly
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Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro
 115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu
 130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu
 145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr
 165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp
 180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val
 195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu
 210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu
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Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
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Arg Ile Ser Ile
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 Val Asn Ser Asp Ser
 1 5

acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
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 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
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gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
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act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
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ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
 120 125 130

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 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
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 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
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Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
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Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
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Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
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Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
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Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
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Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
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Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
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Leu Asn Trp Arg Gly
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Met Tyr Ile Pro Glu 1 5																		
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Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu 10 15 20																		
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Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu 25 30 35																		
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Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His 40 45 50																		
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Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln 55 60 65																		
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Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu 70 75 80 85																		
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Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly 90 95 100																		
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Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn 105 110 115																		
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Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala 135 140 145																		
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Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser 150 155 160 165																		
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Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val	
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1219																
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cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc	
1315																
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser	
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 Ala Glu Ala

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Phe	Val	Ile	Pro	Glu	Ile	Glu	Ala	Leu	Ala	Thr	Asp	Glu	Leu	Val	Lys
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Ile	Glu	Glu	Glu	Gly	Leu	Ala	Thr	Ile	Val	Pro	Thr	Ala	Arg	Ala	Ala
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Asp	Leu	Gln	Ala	Ala	Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala
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Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
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Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
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Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
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Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
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Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val
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 Met Ser Thr Phe Val
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 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
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 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
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Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
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 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala
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 1123
 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val
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 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu
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 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac
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 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn
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 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct
 1267
 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro
 375 380 385
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag
 1315
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln
 390 395 400 405
 ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct
 1363
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala
 410 415 420
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt
 1411
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe
 425 430 435
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca
 1459
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala
 440 445 450
 aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt
 1507
 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg
 455 460 465
 ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag
 1555
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu
 470 475 480 485
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg
 1603
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490										495					500					
gtc tcc acc ggt gca cgc cca gtg gct gtc acc aac tgc ctg aac ttc																				
1651																				
Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe					
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1699																				
Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val	Met	Trp	Gln	Phe	Lys	Glu	Ala	Val					
		520					525					530								
cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc																				
1747																				
His	Gly	Leu	Ala	Asp	Gly	Ser	Lys	Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly					
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1795																				
Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro					
550					555					560					565					
acc cca gtc gtg ggt gtt ttg gga gtc ttg gac aac gtc gag cag agc																				
1843																				
Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	Asn	Val	Glu	Gln	Ser					
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atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt																				
1891																				
Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu	Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly					
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gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc																				
1939																				
Glu	Thr	Phe	Asp	Glu	Phe	Gly	Gly	Ser	Ile	Trp	Gln	Gln	Val	Ser	Gly					
		600					605						610							
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag																				
1987																				
Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro	Val	Val	Asp	Leu	Leu	Asn	Glu	Gln					
	615					620					625									
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac																				
2035																				
Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly	Ser	Asp	Leu	Phe	Ala	Ala	Ser	His					
630					635						640				645					
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc																				
2083																				
Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly	Gln	Thr	Leu	Ala	Glu	Leu	Ala	Ile					
			650					655					660							
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc																				
2131																				
His	Gln	Lys	Lys	Gly	Met	Asp	Val	Asp	Leu	Ser	Gln	Ile	His	Pro	Ser					
			665					670					675							
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca																				
2179																				
Leu	Phe	Thr	Ser	Leu	Phe	Ala	Glu	Ser	Ala	Ser	Arg	Ile	Val	Val	Ala					
		680					685					690								

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt
 2227
 Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
 695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc
 2275
 Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
 710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa
 2323
 Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
 730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct
 2371
 Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
 745 750 755

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 Asn Ala Val Val Ala
 760

<210> 912
 <211> 762
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 912
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 35 40 45
 Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
 50 55 60
 Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
 65 70 75 80
 Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
 85 90 95
 Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
 100 105 110
 Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
 115 120 125
 Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
 130 135 140
 Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145		150		155		160
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu						
		165		170		175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn						
		180		185		190
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu						
		195		200		205
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly						
		210		215		220
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser						
		225		230		235
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val						
		245		250		255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu						
		260		265		270
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly						
		275		280		285
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met						
		290		295		300
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala						
		305		310		315
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val						
		325		330		335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp						
		340		345		350
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr						
		355		360		365
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr						
		370		375		380
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn						
		385		390		395
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val						
		405		410		415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu						
		420		425		430
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly						
		435		440		445
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp						
		450		455		460
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg						
		465		470		475
						480



Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu
 485 490 495
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr
 500 505 510
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln
 515 520 525
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly
 530 535 540
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp
 545 550 555 560
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp
 565 570 575
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp
 580 585 590
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp
 595 600 605
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp
 610 615 620
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu
 625 630 635 640
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu
 645 650 655
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser
 660 665 670
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser
 675 680 685
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala
 690 695 700
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser
 705 710 715 720
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val
 725 730 735
 Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly
 740 745 750
 His Ala Val Gly Ala Asn Ala Val Val Ala
 755 760

<210> 913

<211> 638

<212> DNA

<213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (54)..(638)
 <223> FRXA02805

<400> 913

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                                     Val Phe
                                     1

cct ggc gtt gtt gac ggc att tcc cat tac ggc aac tgc ctc ggc ctg 107
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
      5                                10                                15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
      20                                25                                30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
      35                                40                                45                                50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
      55                                60                                65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
      70                                75                                80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
      85                                90                                95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
      100                                105                                110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
      115                                120                                125                                130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
      135                                140                                145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
      150                                155                                160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
      165                                170                                175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
      180                                185                                190

gtc
Val
195

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<210> 914
 <211> 195
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 914

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Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu
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Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala
              20              25              30

Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu
              35              40              45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
              50              55              60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
              65              70              75              80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val
              85              90              95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
              100             105             110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
              115             120             125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
              130             135             140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
              145             150             155             160

Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala
              165             170             175

Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys
              180             185             190

Trp Asp Val
              195
  
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<210> 915
 <211> 697
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (23)..(697)

<223> FRXA00537

<400> 915

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              Val Tyr His Arg Ala Val Leu Asn Ala Thr
  
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tcc gcg gca aca ccg ttc aag caa aag aac gcc aat gct ggc gtc ttg				100
Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu	15	20	25	
cg t atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca				148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala	30	35	40	
tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca				196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala	45	50	55	
ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg				244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val	60	65	70	
gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt				292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val	75	80	85	90
atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag				340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys	95	100	105	
ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag				388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln	110	115	120	
act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga				436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly	125	130	135	
gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag				484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu	140	145	150	
gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc				532
Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly	155	160	165	170
tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca				580
Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro	175	180	185	
gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt				628
Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly	190	195	200	
tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc				676
Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly	205	210	215	
cag acc ctc gca gag ctt gcg				697
Gln Thr Leu Ala Glu Leu Ala	220	225		

<210> 916

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe
 1 5 10 15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr
 20 25 30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn
 180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
 195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
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Ala
 225

<210> 917

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (1)..(279)

<223> FRXA00561

<400> 917

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Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1             5             10             15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
          20             25             30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35             40             45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50             55             60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65             70             75             80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
          85             90

ctgtgaagcc ggg 302

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<210> 918
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 918
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Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
          20             25             30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35             40             45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50             55             60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65             70             75             80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
          85             90

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<210> 919
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(769)
 <223> RXA00541

<400> 919

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tcacgaaga cttcgaatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115
 Val Ser Ala Lys Ile
 1 5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163
 Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg
 10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211
 Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp
 25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259
 Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser
 40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307
 Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val
 55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355
 Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly
 70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403
 Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly
 90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451
 Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His
 105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499
 Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys
 120 125 130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547
 Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln
 135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595
 Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val
 150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643
 Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly
 170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691
 Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu
 185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739
 His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu
 200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
215 220

act

792

<210> 920

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp
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Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
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<222> (101)..(991)

<223> RXA00620

<400> 921

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                                         Met Arg Pro Glu Leu
                                         1                               5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
                        10                               15                               20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
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tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
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act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
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ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
                        70                               75                               80                               85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
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gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
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agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
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cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
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Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
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Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
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gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
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                        185                               190                               195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

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Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
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cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
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atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
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1014			
Gly Ser Cys Val			
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Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp			
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Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile			
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Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro			
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Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu			
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Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val			
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Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly			
	115	120	125
Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr			
	130	135	140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
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 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
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 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
 225 230 235 240
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
 245 250 255
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
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 Leu Leu Ser Pro Tyr
 1 5
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
 10 15 20
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
 25 30 35
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
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 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

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Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu		
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Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp		
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Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp		
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Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val		
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Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys		
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Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His		
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Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val		
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ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggg	ctg	cac	tcc	aac	ggg	787	
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Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu		
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Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu		
				250					255					260			
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931	
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu		
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tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979	
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly		
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 1075
 Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
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 Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
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 atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg
 1171
 Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met
 345 350 355
 ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac
 1219
 Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
 360 365 370
 ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc
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 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met	Asp	Lys	His	Asp	Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	115	120	125
Asp	Asp	Leu	Val	Val	Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	130	135	140
Ile	Ala	Ile	Gly	Lys	Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	145	150	155
Gly	Ile	Ala	Glu	Gly	Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	165	170	175
Glu	Thr	Ala	Glu	His	Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	180	185	190
Ser	Ala	Thr	Ala	Val	Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	195	200	205
Asp	Arg	Val	Arg	Ala	Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	210	215	220
Leu	His	Ser	Asn	Gly	Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	225	230	235
Ala	Gly	Leu	Ala	Leu	Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	245	250	255
Gly	Glu	Glu	Leu	Leu	Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	260	265	270
Ala	Leu	Ile	Ala	Glu	Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	275	280	285
Gly	Gly	Leu	Ala	Gly	Asn	Leu	Glu	Arg	Val	Val	Pro	Glu	Gly	Leu	Val	290	295	300
Ala	Glu	Met	Ser	Arg	Ala	Thr	Trp	Thr	Pro	Gly	Gln	Ile	Phe	Arg	Thr	305	310	315
Ile	Ser	Ser	Val	Gly	Lys	Val	Ser	Arg	Glu	Glu	Met	Glu	Lys	Thr	Phe	325	330	335
Asn	Met	Gly	Val	Gly	Met	Val	Ala	Val	Val	Ala	Glu	Lys	Asp	Arg	Asp	340	345	350
Arg	Ala	Leu	Ala	Met	Leu	Thr	Ala	Arg	His	Ile	Asp	Cys	Trp	Glu	Ile	355	360	365
Gly	Thr	Val	Arg	Asn	Gly	Glu	Glu	Gly	Glu	Pro	Arg	Val	Ile	Leu	Asn	370	375	380
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gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
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gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
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Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
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Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
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Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
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Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
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 225 230 235

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 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu
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gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818
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Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
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Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
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Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
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Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
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Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
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Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
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ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240
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 65 70 75 80

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 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
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aag 338

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<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

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Lys	Thr	Phe	Asn	Met	Gly	Val	Gly	Met	Val	Ala	Val	Val	Ala	Glu	Lys
	50					55					60				
Asp	Arg	Asp	Arg	Ala	Leu	Ala	Met	Leu	Thr	Ala	Arg	His	Ile	Asp	Cys
	65				70					75					80
Trp	Glu	Ile	Gly	Thr	Val	Arg	Asn	Gly	Glu	Glu	Gly	Glu	Pro	Arg	Val
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aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac																163
<div>Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp</div> <div>10 15 20</div>																
ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa																211
<div>Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln</div> <div>25 30 35</div>																
tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta																259
<div>Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val</div> <div>40 45 50</div>																
gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc																307
<div>Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg</div> <div>55 60 65</div>																
gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc																355
<div>Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val</div> <div>70 75 80 85</div>																
ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag																403
<div>Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln</div> <div>90 95 100</div>																
cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc																451

Pro Arg Pro	Glu Ala Leu Val	Asn Ala Gln Asp Lys Leu Val	Met Arg	
	105	110	115	
aag cgt cta cgt gaa ctc ggc gca cca gtc cca cca ttt gct gcc att				499
Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro Pro Phe Ala Ala Ile	120	125	130	
gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca gtt gat ggc caa				547
Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala Val Asp Gly Gln	135	140	145	
gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc aag ggc gta tgg				595
Val Cys Leu Lys Ala Arg Glu Gly Tyr Asp Gly Lys Gly Val Trp	150	155	160	165
ttc cca gcc gat gta gca gag ctt cag tgc ctt gtg gca gag ctt ctc				643
Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val Ala Glu Leu Leu	170	175	180	
gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt gcc ctc aac agg				691
Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val Ala Leu Asn Arg	185	190	195	
gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga gaa acc aaa gcg				739
Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly Glu Thr Lys Ala	200	205	210	
tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg tgt gca gaa gca				787
Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val Cys Ala Glu Ala	215	220	225	
atc gct ccc gca cct gaa cta tcc gca gaa ctg cag gaa tcc acc aga				835
Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln Glu Ser Thr Arg	230	235	240	245
gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc act ggt gtc ttg				883
Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val Thr Gly Val Leu	250	255	260	
gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg cag cca gag atc				931
Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly Gln Pro Glu Ile	265	270	275	
ttt gtc aac gag ctc gcc atg cgt tca cac aac acc ggc cac tgg act				979
Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr Gly His Trp Thr	280	285	290	
caa gat ggc tgc gtg acc agc caa ttc gag cag cac ctc cgc gca gtc				
1027				
Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His Leu Arg Ala Val	295	300	305	
ctc gac tac cca ctg ggt gct acc gac act ttg gct gat tac acc gtg				
1075				
Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala Asp Tyr Thr Val	310	315	320	325
atg gcc aac gtg ctc ggt gcc gac acc gac cca gag atg ccc atg gca				
1123				
Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu Met Pro Met Ala	330	335	340	

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac
 1171
 Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
 345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac
 1219
 Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
 360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc
 1267
 Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
 375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgccta
 1317
 Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 390 395

gca
 1320

<210> 930
 <211> 399
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 930
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 Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala
 20 25 30
 Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
 35 40 45
 Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
 50 55 60
 Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
 65 70 75 80
 Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
 85 90 95
 Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
 100 105 110
 Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
 115 120 125
 Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
 130 135 140
 Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp
 145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
 165 170 175
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
 180 185 190
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
 195 200 205
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
 210 215 220
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
 225 230 235 240
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
 245 250 255
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
 260 265 270
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
 275 280 285
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
 290 295 300
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu
 305 310 315 320
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro
 325 330 335
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro
 340 345 350
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
 355 360 365
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala
 370 375 380
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 385 390 395

<210> 931

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(810)

<223> FRXA02345

<400> 931

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gtt gat ggc caa gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc	96
Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tgc ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg	288
Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa	768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 260 265 270

taggtctttt ctgagcgcta gca

833

<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

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Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly
 20 25 30

Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val
 35 40 45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val
 50 55 60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala
 180 185 190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu
 195 200 205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
 225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
 245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp



260

265

270

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<213> Corynebacterium glutamicum
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<223> RXN02350
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ataaacccgat acgtactttt cgcgccttaag gagaattttca gtg ggt cct cta gtt 115
Val Gly Pro Leu Val
1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
25 30 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala
40 45 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala
55 60 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly
 70 75 80 85

ggt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser
90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly
105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499
Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly
120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala
135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
150 155 160 165

taatqaatcc gatcgtggtg ctg 618

<210> 934
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 934
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 Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
 20 25 30
 Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
 35 40 45
 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
 50 55 60
 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
 65 70 75 80
 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
 85 90 95
 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
 100 105 110
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
 115 120 125
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
 130 135 140
 Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
 145 150 155 160
 Lys Arg Leu Leu Gly
 165

<210> 935
 <211> 223
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(223)
 <223> FRXA02346

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 ataaaccgat acgtaacttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115
 Val Gly Pro Leu Val
 1 5
 ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

	10	15	20	
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc				211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
	25	30	35	
tct gca cac cgc				223
Ser Ala His Arg				
	40			
<210> 936				
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<212> PRT				
<213> Corynebacterium glutamicum				
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Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp				
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Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe				
20 25 30				
Glu Val Gly Val Val Ser Ala His Arg				
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<210> 937				
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<223> FRXA02350				
<400> 937				
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Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro				
1 5 10				
ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca				100
Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala				
15 20 25				
ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc				148
Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
30 35 40				
acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc				196
Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
45 50 55				
aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg				249
Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly				
60 65 70				
ctg				252



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<210> 938
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<212> PRT
<213> Corynebacterium glutamicum
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      20              25              30
Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp
      35              40              45
Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu
      50              55              60
Lys Lys Arg Leu Leu Gly
 65              70

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<213> Corynebacterium glutamicum
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<223> RXA01087
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Met Gln Thr Leu Ala															
1 5															
gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat															163
Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp															
10 15 20															
ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc															211
Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala															
25 30 35															
gga gtg cgc cac act gac gca att gtt cgt gat cag att tac cca act															259
Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr															
40 45 50															
ttt ctt ccc gca gtt ttc ggc cac gaa ggc gcc gga gta gtt gtc gcc															307
Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala															
55 60 65															
gtg ggt tct gca gtc acc tcg gtg aaa cca gat gac aag gta gtg ctg															355
Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu															
70 75 80 85															
gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct															403
Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro															

	90	95	100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat				451
Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp				
	105	110	115	
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag				499
Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu				
	120	125	130	
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt				547
Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly				
	135	140	145	
ttc ctg gca tac cca gca act ccc cca gag gct tcg gga gta agc gtg				595
Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val				
	150	155	160	165
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca				643
Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala				
	170	175	180	
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat				691
Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp				
	185	190	195	
ttt gga gtg gct ggc atc cac cgc ctg ctt tca tac gaa gaa gaa ctc				739
Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu				
	200	205	210	
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta				787
Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu				
	215	220	225	
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca				835
Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro				
	230	235	240	245
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg				883
Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu				
	250	255	260	
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat				931
Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp				
	265	270	275	
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg				976
Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg				
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<210> 940

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 940

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Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile
 20 25 30
 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp
 35 40 45
 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala
 50 55 60
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
 65 70 75 80
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
 85 90 95
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe
 100 105 110
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr
 115 120 125
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr
 130 135 140
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala
 145 150 155 160
 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro
 165 170 175
 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr
 180 185 190
 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser
 195 200 205
 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly
 210 215 220
 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro
 225 230 235 240
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly
 245 250 255
 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly
 260 265 270
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln
 275 280 285
 Ile Ala Ala Arg
 290

<210> 941

<211> 1551

<212> DNA

<213> *Corynebacterium glutamicum*

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 <222> (101)..(1528)
 <223> RXA00619

<400> 941

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 Val Ala Asp Lys Lys
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aag atc gca aac gtc ctg tct aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
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aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
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atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
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agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
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atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
 90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
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acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
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ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
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caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

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Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp		
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Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
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Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile		
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cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggt	ttt	aag	gaa	ggc	931	
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly		
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Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
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Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
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1123																	
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp		
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gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggt	gca	ttc		
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			345					350					355				
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca		
1219																	
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
		360					365					370					
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
1267																	
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
	375					380					385						
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac		
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390					395				400						405		
atg	cgc	gaa	aat	ggc	ggt	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
1363																	
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 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
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 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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 <213> *Corynebacterium glutamicum*

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 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
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 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
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 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
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<211> 1683

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1660)

<223> RXA02622

<400> 943

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Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
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gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
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acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
                        40                45                50

ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
                        55                60                65

aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
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aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
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cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
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ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
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tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
                        135                140                145

gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
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gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
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cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

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acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787																			
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln																				
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Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys																				
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gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931																			
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Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile																				
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1123																				
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu																				
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1219																				
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser																				
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ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac																				
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aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag																				
1315																				
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu																				
390 395 400 405																				

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1363
Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys
410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc
1411
Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly
425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt
1459
Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg
440 445 450

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Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
455 460 465

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1555
Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
470 475 480 485

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1603
Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac
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Phe Ala His
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<210> 944

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

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35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu
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 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala
 100 105 110
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile
 115 120 125
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro
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 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu
 145 150 155 160
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala
 165 170 175
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr
 180 185 190
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro
 195 200 205
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly
 210 215 220
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly
 225 230 235 240
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn
 245 250 255
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg
 260 265 270
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val
 275 280 285
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp
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 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser
 305 310 315 320
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile
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 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys
 340 345 350
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu
 355 360 365
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile
 370 375 380
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser
 385 390 395 400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp
 485 490 495

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Thr Gly Ala Arg His Phe Ala His
 515 520

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1618)
 <223> RXN00488

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 Met Thr Thr Gln Ser
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
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atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
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Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
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Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
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 Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His
 330 335 340
 aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt
 1171
 Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly
 345 350 355
 gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc
 1219
 Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly
 360 365 370
 tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc
 1267
 Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile
 375 380 385
 aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct
 1315
 Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala
 390 395 400 405
 atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac
 1363
 Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
 410 415 420
 cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa
 1411
 Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
 425 430 435
 ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att
 1459
 Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
 440 445 450
 cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc
 1507
 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
 455 460 465
 tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc
 1555
 Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
 470 475 480 485
 gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa
 1603
 Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
 490 495 500
 gct cct aac tac cac tagattttgc tcaacttaaagc
 1641
 Ala Pro Asn Tyr His
 505

<210> 946

<211> 506

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 946

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Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
      20                      25                      30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
      35                      40                      45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
      50                      55                      60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
      65                      70                      75                      80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
      85                      90                      95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
      100                      105                      110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
      115                      120                      125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
      130                      135                      140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
      145                      150                      155                      160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
      165                      170                      175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
      180                      185                      190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
      195                      200                      205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
      210                      215                      220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
      225                      230                      235                      240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
      245                      250                      255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
      260                      265                      270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
      275                      280                      285

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Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala
 290 295 300
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg
 305 310 315 320
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala
 325 330 335
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly
 340 345 350
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn
 355 360 365
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
 370 375 380
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
 420 425 430
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
 435 440 445
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
 450 455 460
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
 465 470 475 480
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile
 485 490 495
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His
 500 505

<210> 947

<211> 574

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA00492

<400> 947

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115

Met Thr Thr Gln Ser

1

5


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cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
          10                      15                      20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
Leu Thr Phe Asp Asp Val Leu Leu Pro Asp Ala Ser Asp Val Val
          25                      30                      35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
          40                      45                      50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
          55                      60                      65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
          70                      75                      80                      85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
          90                      95                      100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
          105                      110                      115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
          120                      125                      130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
          135                      140                      145

cgc gat atg cgt ttt gaa agc gac atg 574
Arg Asp Met Arg Phe Glu Ser Asp Met
          150                      155

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<210> 948

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 948

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Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
  1                      5                      10                      15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
          20                      25                      30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
          35                      40                      45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
          50                      55                      60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
          65                      70                      75                      80

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Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met
 145 150 155

<210> 949

<211> 557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(534)

<223> FRXA00488

<400> 949

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Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly	
1 5 10 15	
ggt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct	96
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala	
20 25 30	
aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg	144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu	
35 40 45	
gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag	192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys	
50 55 60	
cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc	240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly	
65 70 75 80	
cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc	288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe	
85 90 95	
cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa	336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu	
100 105 110	
ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag	384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln	
115 120 125	
gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att	432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557
 Tyr His

<210> 950
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 950
 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
 1 5 10 15

Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

Tyr His

<210> 951
 <211> 1554



<212> DNA
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101) .. (1531)
<223> RXA02469
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<400> 951																
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gccgtgttca gggataactg attaatcaac taggagaccc atg cgt ttt ctt aac																115
Met Arg Phe Leu Asn																5
1																
aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg																163
Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val																20
10 15																
cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc																211
Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr																35
25 30																
aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act																259
Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr																50
40 45																
gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc																307
Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly																65
55 60																
atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act																355
Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr																85
70 75																
atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc																403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr																100
90 95																
gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag																451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys																115
105 110																
cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc																499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly																130
120 125																
atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg																547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val																145
135 140																
ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc																595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser																165
150 155																
ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc																643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala																180
170 175																
ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc																691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr																

185	190	195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc			739
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly			
200	205	210	
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga			787
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly			
215	220	225	
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac			835
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp			
230	235	240	245
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc			883
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile			
250	255	260	
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc			931
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr			
265	270	275	
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag			979
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys			
280	285	290	
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc			
1027			
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly			
295	300	305	
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc			
1075			
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala			
310	315	320	325
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc			
1123			
Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro			
330	335	340	
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc			
1171			
Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val			
345	350	355	
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc			
1219			
Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe			
360	365	370	
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg			
1267			
Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg			
375	380	385	
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca			
1315			
Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala			
390	395	400	405

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att
 1363
 Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile
 410 415 420
 gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc
 1411
 Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser
 425 430 435
 ggt gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc
 1459
 Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr
 440 445 450
 ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca
 1507
 Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala
 455 460 465
 gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga
 1554
 Glu Gly Lys Pro Arg Ala Ser Arg
 470 475

<210> 952
 <211> 477
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 952
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 20 25 30
 Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val
 35 40 45
 Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile
 50 55 60
 Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp
 65 70 75 80
 Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe
 85 90 95
 Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg
 100 105 110
 Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly
 115 120 125
 Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp
 130 135 140
 Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu
 145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His
 165 170 175
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly
 180 185 190
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala
 195 200 205
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn
 210 215 220
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp
 225 230 235 240
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser
 245 250 255
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala
 260 265 270
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly
 275 280 285
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr
 290 295 300
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu
 305 310 315 320
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly
 325 330 335
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala
 340 345 350
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro
 355 360 365
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe
 370 375 380
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu
 385 390 395 400
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr
 405 410 415
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
 420 425 430
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
 435 440 445
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser
 450 455 460
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg
 465 470 475

<210> 953
 <211> 1692
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1669)
 <223> RXN00487

<400> 953
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 agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115
 Val Ser Leu Gln Thr
 1 5
 aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
 10 15 20
 ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
 25 30 35
 ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
 40 45 50
 ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
 55 60 65
 tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att 355
 Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile
 70 75 80 85
 tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc 403
 Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala
 90 95 100
 aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt 451
 Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly
 105 110 115
 ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc 499
 Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser
 120 125 130
 cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg 547
 His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala
 135 140 145
 tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa 595
 Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys
 150 155 160 165
 atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc 643
 Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly
 170 175 180

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	
1075	
Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
310 315 320 325	
tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg	
1123	
Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
330 335 340	
gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac	
1171	
Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
345 350 355	
gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg	
1219	
Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu	
360 365 370	
cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc	
1267	
Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly	
375 380 385	
ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt	
1315	

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405
 ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420
 cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435
 gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450
 tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg
 1507
 Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val
 455 460 465
 ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc
 1555
 Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg
 470 475 480 485
 ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa
 1603
 Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu
 490 495 500
 gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca
 1651
 Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro
 505 510 515
 gga acc atc gaa tgg gag taggccttaa atgagccttc gtt
 1692
 Gly Thr Ile Glu Trp Glu
 520

<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
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 20 25 30
 Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
 35 40 45
 Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
 50 55 60



Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
 65 70 75 80
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
 85 90 95
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
 405 410 415
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
 420 425 430
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
 435 440 445
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
 450 455 460
 Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
 465 470 475 480
 Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
 485 490 495
 Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val
 500 505 510
 Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
 515 520

<210> 955
 <211> 1486
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1486)
 <223> FRXA00487

<400> 955
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 Val Ser Leu Gln Thr
 1 5
 aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
 10 15 20
 ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
 25 30 35
 ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
 40 45 50
 ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
 55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
 1075
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
 1123
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
 1171
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
 1219
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
 1315
 Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc
 1486
 Ser Val Gly Val Gln Gly Asp Gly Arg
 455 460

<210> 956
 <211> 462
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 956
 Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
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 Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

20										25					30				
Tyr	Ser	Glu	Val	Ile	Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala				
		35					40					45							
Lys	Asn	Ala	Ala	Ala	Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr				
	50					55					60								
Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu				
65					70					75					80				
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu				
				85					90					95					
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp				
			100					105					110						
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His				
		115					120					125							
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly				
	130					135					140								
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu				
145					150					155					160				
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu				
				165					170					175					
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile				
			180					185					190						
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu				
		195					200					205							
Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys				
	210					215					220								
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln				
225					230					235					240				
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu				
				245					250					255					
Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala				
			260				265						270						
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser				
		275					280					285							
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly				
	290					295					300								
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu				
305					310					315					320				
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu				
				325					330					335					
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile				
			340					345					350						

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
 405 410 415
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
 420 425 430
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
 435 440 445
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg
 450 455 460

<210> 957
 <211> 693
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(670)
 <223> RXA02237

<400> 957
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 gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115
 Val Ser Gly Asp Asn
 1 5
 caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys
 10 15 20
 tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe
 25 30 35
 agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly
 40 45 50
 cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp
 55 60 65
 tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg
 70 75 80 85
 tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg
 90 95 100

cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser
 105 110 115

tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu
 120 125 130

gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val
 135 140 145

att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser
 150 155 160 165

gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys
 170 175 180

gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggg 690
 Ala Ile Glu Asp Val Leu Leu Gly Ala
 185 190

agg 693

<210> 958

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 958

Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro
 1 5 10 15

Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val
 20 25 30

Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro
 35 40 45

Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe
 50 55 60

Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His
 65 70 75 80

Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala
 85 90 95

Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala
 100 105 110

Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala
 115 120 125

Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr

130 135 140

Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu
 145 150 155 160

Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val
 165 170 175

Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala
 180 185 190

<210> 959
 <211> 1413
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1390)
 <223> RXA01446

<400> 959
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tgcatactcc aacttcattg atcggatgtg acgtaaacca atg gct gca atc gtt 115
 Met Ala Ala Ile Val
 1 5

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163
 Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp
 10 15 20

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211
 Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn
 25 30 35

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259
 Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys
 40 45 50

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307
 Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly
 55 60 65

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355
 Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly
 70 75 80 85

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403
 Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn
 90 95 100

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451
 Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu
 105 110 115

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499
 Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly
 120 125 130

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac
 1027
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac
 1075
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca
 1123
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca
 1171
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg
1219

Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt
1267

Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt
1315

Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc
1363

Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt
1410

Val Leu His Asp Val Leu Ala Asp Asn
425 430

gag
1413

<210> 960

<211> 430

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 960

Met Ala Ala Ile Val Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys
1 5 10 15

Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys
20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu
35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala
50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe
65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu
85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met
100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr
115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly
130 135 140

Ile	Arg	Val	Gln	Asp	Ile	Phe	Asp	Glu	Ser	Ile	Leu	Arg	Gln	Lys	Val	145	150	155	160
Glu	Ser	Ala	Leu	Asp	Tyr	Lys	Asn	Gln	Val	Leu	Val	Lys	Met	Tyr	Asn	165	170		175
Arg	Lys	Ala	Ile	Val	Ala	Glu	Glu	Ile	Val	Gln	Tyr	Phe	Leu	Ser	Tyr	180	185		190
Ala	Asp	Arg	Leu	Arg	Pro	Met	Val	Ile	Asp	Ala	Thr	Leu	Val	Leu	Asn	195	200		205
Glu	Ala	Leu	Asp	Gln	Gly	Lys	His	Val	Leu	Met	Glu	Gly	Gly	Gln	Ala	210	215		220
Thr	Met	Leu	Asp	Val	Asp	His	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	225	230	235	240
Asn	Pro	Thr	Ala	Gly	Gly	Ala	Ser	Val	Gly	Ser	Gly	Ile	Gly	Pro	Thr	245	250		255
Lys	Ile	Thr	Ser	Ser	Leu	Gly	Ile	Ile	Lys	Ala	Tyr	Thr	Thr	Arg	Val	260	265		270
Gly	Ala	Gly	Pro	Phe	Pro	Thr	Glu	Leu	Phe	Asp	Lys	Trp	Gly	Glu	Tyr	275	280		285
Leu	Gln	Thr	Val	Gly	Gly	Glu	Val	Gly	Val	Asn	Thr	Gly	Arg	Lys	Arg	290	295	300	
Arg	Cys	Gly	Trp	Tyr	Asp	Ser	Val	Ile	Ala	Arg	Tyr	Ala	Ser	Arg	Val	305	310	315	320
Asn	Gly	Phe	Thr	Asp	Tyr	Phe	Leu	Thr	Lys	Leu	Asp	Val	Leu	Thr	Gly	325	330		335
Ile	Gly	Glu	Ile	Pro	Ile	Cys	Val	Ala	Tyr	Asp	Val	Asp	Gly	Val	Arg	340	345		350
His	Asp	Glu	Met	Pro	Leu	Thr	Gln	Ser	Glu	Phe	His	His	Ala	Thr	Pro	355	360		365
Ile	Phe	Glu	Thr	Met	Pro	Ala	Trp	Asp	Glu	Asp	Ile	Thr	Asp	Cys	Lys	370	375	380	
Thr	Phe	Glu	Asp	Leu	Pro	Gln	Lys	Ala	Gln	Asp	Tyr	Val	Arg	Arg	Leu	385	390	395	400
Glu	Glu	Leu	Ser	Gly	Ala	Arg	Phe	Ser	Tyr	Ile	Gly	Val	Gly	Pro	Gly	405	410		415
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<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<400> 961

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 Val Ala Asp Lys Lys
 1 5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
 10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
 25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
 55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
 70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
 90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
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acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
 170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
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 185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

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Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp		
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Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
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gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883	
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile		
				250					255					260			
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggc	ttt	aag	gaa	ggc	931	
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly		
			265					270					275				
cag	gtc	ggc	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979	
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
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gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg		
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Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met		
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gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc		
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Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
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Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
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act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
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Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
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acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gca	gtt	gcc	ctc	aac		
	1315																
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn		
	390				395				400						405		
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
	1363																
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410 415 420
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
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 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435
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 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450
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 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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 Tyr Arg Pro Gly Glu Ile Leu
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
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 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
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 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
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 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
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 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
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 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
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<211> 666



<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00688

<400> 963

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                                         Met Arg Leu Val Leu
                                         1           5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
                        10                      15                      20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
                        25                      30                      35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
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Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
                        55                      60                      65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
                        70                      75                      80                      85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
                        90                      95                      100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
                        105                      110                      115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
                        120                      125                      130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
                        135                      140                      145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
                        150                      155                      160                      165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
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 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
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 Lys Ala Leu Gly Lys
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 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
 10 15 20
 atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
 25 30 35
 ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
 40 45 50
 gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
 55 60 65
 cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
 70 75 80 85
 cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
 90 95 100
 acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
 105 110 115
 ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
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 cct aac ctg taatttttac ggtagaaaa aaa 531
 Pro Asn Leu
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<210> 966

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 966

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 35 40 45
 His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60
 Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80
 Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
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Ile Ser Ile Trp Phe Pro Asn Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1222)
 <223> RXA00489

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 Met Arg Asp His Val
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259
 Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
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cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala 170 175 180			643
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ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala 230 235 240 245			835
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile 250 255 260			883
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tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			



360

365

370

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1245
Asn

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<212> PRT
<213> Corynebacterium glutamicum
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20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp
35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe
50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu
65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val
85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu
100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg
115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser
130 135 140

Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala
145 150 155 160

Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn
165 170 175

Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp
180 185 190

Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His
195 200 205

Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn
210 215 220

Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile
225 230 235 240

Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly
245 250 255



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						Val	Gln	Lys	Asp	Ser						
						1				5						
gtg	gtg	cgc	atg	gaa	gca	aca	acg	atc	gat	gac	gca	atc	gcg	aag	ctc	163
Val	Val	Arg	Met	Glu	Ala	Thr	Thr	Ile	Asp	Asp	Ala	Ile	Ala	Lys	Leu	
				10					15					20		
att	gac	atc	tac	gac	acc	tcg	acc	aaa	ctg	gcc	aaa	gaa	acc	ctc	aac	211
Ile	Asp	Ile	Tyr	Asp	Thr	Ser	Thr	Lys	Leu	Ala	Lys	Glu	Thr	Leu	Asn	
			25				30				35					
aat	gag	gac	tac	gcc	gca	tac	gcc	gat	gtt	gtt	tac	ccc	aaa	ctc	acc	259
Asn	Glu	Asp	Tyr	Ala	Ala	Tyr	Ala	Asp	Val	Val	Tyr	Pro	Lys	Leu	Thr	
			40				45				50					
gtt	gac	gtg	ctg	gaa	tgg	aaa	ccc	atc	gac	cgc	acc	gaa	ccc	ttc	ggc	307
Val	Asp	Val	Leu	Glu	Trp	Lys	Pro	Ile	Asp	Arg	Thr	Glu	Pro	Phe	Gly	
		55			60			65								
tat	gtg	gat	cga	gcc	ggg	cga	tac	tcc	gcc	acc	ttg	tcc	aaa	cca	cgc	355
Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg	

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403			
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn				
90	95	100		
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451			
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro				
105	110	115		
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499			
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly				
120	125	130		
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547			
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp				
135	140	145		
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595			
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro				
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ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643			
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile				
170	175	180		
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691			
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu				
185	190	195		
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739			
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met				
200	205	210		
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787			
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro				
215	220	225		
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835			
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu				
230	235	240	245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883			
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
250	255	260		
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931			
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
265	270	275		
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979			
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
280	285	290		
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				
1027				
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
295	300	305		
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				
1075				

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325
 ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340
 atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
 1171
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355
 aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
 1219
 Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370
 tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
 1267
 Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385
 acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
 1315
 Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405
 tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
 1363
 Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420
 cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
 1411
 Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435
 ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
 1459
 Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450
 tac ctg gca gta gat cct gaa ccg ttg cgt acc cgt aaa ctg cgc agg
 1507
 Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
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 Thr Leu Gly Glu Val Pro Phe Arg
 470 475

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
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<211> 1191

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1168)

<223> FRXA02281

<400> 971

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cctataaaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser 5
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc	355
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg	
70 75 80 85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	
1027	
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att
1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

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1191

<210> 972

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
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 Ile Tyr Gly Ser
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1279)
 <223> RXA00147

<400> 973
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 Val Ser Lys Asp Thr
 1 5
 acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
 10 15 20
 gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile
 25 30 35
 ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr		
		40					45					50					
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307	
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala		
	55					60					65						
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355	
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu		
	70				75					80					85		
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Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu		
				90					95					100			
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451	
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu		
			105					110					115				
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Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala		
		120					125					130					
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggc	tcc	att	gca	gcg	ggc	atc	ttc	547	
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe		
	135					140					145						
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595	
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val		
	150				155					160					165		
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643	
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser		
				170					175					180			
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691	
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr		
			185				190						195				
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739	
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe		
		200				205						210					
tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787	
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe		
	215					220					225						
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835	
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly		
	230				235					240					245		
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883	
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu		
				250				255						260			
gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931	
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln		
			265				270						275				
att	ctt	ggc	cgc	gca	ttc	ggc	atg	gag	acc	tac	aag	ctg	aag	ttc	ggc	979	
Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly		



280 285 290
 cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305
 gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325
 cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340
 ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
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 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
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 Lys Lys Gly Ala
 390

<210> 974
 <211> 393
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 974
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 35 40 45
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
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 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
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 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
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 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(1036)

<223> RXA00145

<400> 975

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                                         Met Lys His Leu Leu
                                         1           5

tcc att agc gat ctt tcc aaa gat gag att gtt gga ttg ctg gat gaa 163
Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
                        10                        15                        20

gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
                        25                        30                        35

ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
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acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
                        55                        60                        65

gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
                        70                        75                        80                        85

tcg ctg aaa gat acc ggc ttg act ttg tcg gca atc ggc gcg gat gcg 403
Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
                        90                        95                        100

atc atc atg cgc cac cca gcc tca ggc gcc gcg cag cag ctt gcg cag 451
Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
                        105                        110                        115

ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
                        120                        125                        130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
                        135                        140                        145

cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
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gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
                        170                        175                        180

act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

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Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu			
215	220	225	
cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg			835
Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu			
230	235	240	245
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc			883
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile			
250	255	260	
atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag			931
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln			
265	270	275	
gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt			979
Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly			
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1027			
Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp			
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Ala Thr Ile			
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Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu			
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Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly			
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Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser			
65	70	75	80
Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala			
85	90	95	

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
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 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
 115 120 125
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
 130 135 140
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
 145 150 155 160
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
 165 170 175
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
 180 185 190
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
 195 200 205
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
 210 215 220
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
 225 230 235 240
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
 245 250 255
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
 260 265 270
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
 275 280 285
 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu
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<211> 1464

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1441)

<223> RXA00146

<400> 977

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 Val Val Asp Ser Asn
 1 5
 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser	
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ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn	
			25					30					35			
gtg	ttt	gtt	aaa	gat	ggc	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu	
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gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggc	ttc	307
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe	
	55					60					65					
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Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu	
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acc	att	gcc	act	ggc	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala	
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gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile	
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gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val	
		120					125					130				
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His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr	
	135					140					145					
gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595
Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser	
	150				155			160							165	
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu	
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gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp	
			185					190					195			
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggc	gaa	aac	gca	gct	739
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala	
		200					205					210				
cgt	ctg	ggc	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val	
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gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile	
	230				235			240							245	
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys	

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Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn				
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ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt				
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ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt				
1075 Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly				
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1171 Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr				
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375 380 385				
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1315 Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala				
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1363 Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly				
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425 430 435				
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1464

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<211> 447
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 978

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Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
		35					40					45			
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55					60				
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
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Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
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Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
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Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
	130					135					140				
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
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Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
		195					200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
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Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
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Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
			260					265					270		

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala
 275 280 285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
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Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val
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Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala
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<210> 979

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<213> Corynebacterium glutamicum

<220>

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<222> (1) .. (1002)

<223> RXA02208

<400> 979

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Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
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Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
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Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
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Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
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acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
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Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
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gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
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Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
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Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac
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Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn
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<210> 980

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 980

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 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225	230	235	240
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	245	250	255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	260	265	270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	275	280	285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	290	295	300
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg	305	310	315
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn	325	330	

<210> 981
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> RXA01660

<400> 981
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 taaacctcaa tcatcaaatt aggggaagggc tgggaaatcc atg tca tct aat tcc 115
 Met Ser Ser Asn Ser
 1 5
 att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu
 10 15 20
 gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp
 25 30 35
 tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg
 40 45 50
 ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp
 55 60 65
 gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile
 70 75 80 85
 atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu
 90 95 100



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gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451
Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
      105                      110                      115

ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499
Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
      120                      125                      130

cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547
Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
      135                      140                      145

ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595
Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
      150                      155                      160                      165

gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643
Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu
      170                      175                      180

gga ctc aac taacaccccc ggccccacgg agt 675
Gly Leu Asn

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<210> 982
 <211> 184
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 982
Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu
  1          5          10          15

Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
      20          25          30

Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
      35          40          45

Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
      50          55          60

Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
      65          70          75          80

Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
      85          90          95

Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
      100         105         110

Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
      115         120         125

Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
      130         135         140

Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
      145         150         155         160

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Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn
 180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

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 cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115
 Met Thr Phe Gly Glu
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val
 135 140 145



ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln
 150 155 160 165

 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala
 170 175 180

 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly
 185 190 195

 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu
 200 205 210

 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala
 215 220 225

 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
 230 235 240 245

 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
 250 255 260

 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
 265 270 275

 tca tagtcgcgga aacggccctt aat 957
 Ser

<210> 984

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg
 1 5 10 15

 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly
 20 25 30

 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val
 35 40 45

 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe
 50 55 60

 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
 65 70 75 80

 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95



Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp
 100 105 110
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu
 115 120 125
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly
 130 135 140
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu
 145 150 155 160
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile
 165 170 175
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys
 180 185 190
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro
 195 200 205
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala
 210 215 220
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala
 225 230 235 240
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro
 245 250 255
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe
 260 265 270
 Pro Gly Phe Pro Arg Ser
 275

<210> 985

<211> 852

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(829)

<223> RXN01892

<400> 985

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 aaagcggttg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115
 Val Thr Thr Ser Ser
 1 5
 gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
 10 15 20
 gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211
 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
 25 30 35

aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att	259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile	
40 45 50	
gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag	307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln	
55 60 65	
cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc	355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly	
70 75 80 85	
aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc	403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly	
90 95 100	
gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa	451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu	
105 110 115	
cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt	499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val	
120 125 130	
gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc	547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr	
135 140 145	
act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg	595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met	
150 155 160 165	
gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca	643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro	
170 175 180	
gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag	691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys	
185 190 195	
ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac	739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn	
200 205 210	
aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct	787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala	
215 220 225	
cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc	829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser	
230 235 240	
tgatacattt agtcttataa aca	852

<210> 986

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
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 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
 20 25 30
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240
 Val Glu Ser

<210> 987

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (47) .. (775)

<223> FRXA01892

<400> 987

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 Val Thr Thr Ser
 1

agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106
 Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu
 5 10 15 20

ggt gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154
 Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val
 25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202
 Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu
 40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
 Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
 55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
 Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
 70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
 Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
 85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
 Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
 105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
 Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
 120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490
 Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
 135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
 Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
 150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586
 Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
 165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
 Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
 185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
 Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
 200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
 Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
 215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
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Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240

Val Glu Ser



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<210> 989
<211> 798
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(775)
<223> RXA00105
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cgaggagaat ggaacttact aacgctgtta tgatgacggc																	
Met Thr Val Pro Thr																	115
1 5																	
cct tat gaa gac ctt ctt cgg aag att gct gaa gaa ggg tcc cac aag	163																
Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu Glu Gly Ser His Lys																	
10 15 20																	
gac gac cgc acc ggc acc ggc act act tct tta ttc gga caa caa atc	211																
Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu Phe Gly Gln Gln Ile																	
25 30 35																	
cgc ttt gat ctc aat gaa ggt ttt ccc ctt ctg acc acc aag aag gtc	259																
Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu Thr Thr Lys Lys Val																	
40 45 50																	
cat ttc cac tct gtt gtg ggt gag ctt ttg tgg ttc ctt cag ggg gat	307																
His Phe His Ser Val Val Gly Glu Leu Leu Trp Phe Leu Gln Gly Asp																	
55 60 65																	
tcc aac gtc aaa tgg ctg cag gat aac aac atc cgc att tgg aat gaa	355																
Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile Arg Ile Trp Asn Glu																	
70 75 80 85																	
tgg gca gat gag gac ggc gag ctg ggc cct gtt tat ggt gtc cag tgg	403																
Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val Tyr Gly Val Gln Trp																	
90 95 100																	
cgt tct tgg cca acc cct gat ggt cgt cac att gac cag atc tca ggt	451																
Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile Ser Gly																	
105 110 115																	
gct tta gaa act ctg cga aac aac cct gat tca cgt cgc aat att gtc	499																
Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser Arg Arg Asn Ile Val																	
120 125 130																	
tcg gcg tgg aat gtt tcc gag ctt gaa aac atg gct ctt ccc cct tgt	547																
Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met Ala Leu Pro Pro Cys																	
135 140 145																	
cac ttg ctt ttc cag ctc tat gtc gcc gat ggc aaa ctg tct tgc cag	595																
His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly Lys Leu Ser Cys Gln																	
150 155 160 165																	
ctc tac cag cgt tct gcg gac atg ttc ctg ggt gtg cct ttc aac atc	643																
Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly Val Pro Phe Asn Ile																	
170 175 180																	

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu
 185 190 195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp
 200 205 210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg
 215 220 225

cctacccac ctt 798

<210> 990

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 990

Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu
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Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu
 20 25 30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu
 35 40 45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
 50 55 60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
 65 70 75 80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
 85 90 95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
 100 105 110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
 115 120 125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
 130 135 140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
 145 150 155 160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
 165 170 175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
 180 185 190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
 195 200 205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg
225

<210> 991
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA00131

<400> 991
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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115
Met Ile Val Ser Ile
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150 155 160 165
 cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg 643
 His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val
 170 175 180
 gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa 691
 Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu
 185 190 195
 ttc ctg ggt act ata aac taatcccaat tagcaggaag gat 732
 Phe Leu Gly Thr Ile Asn
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<210> 992
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 992
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 Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His
 35 40 45
 Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu
 50 55 60
 Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly
 65 70 75 80
 Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala
 85 90 95
 Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu
 100 105 110
 Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp
 115 120 125
 Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu
 130 135 140
 Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln
 145 150 155 160
 Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu
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 Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala
 180 185 190
 Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn
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<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(508)  
<223> RXA00266
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Met Thr Glu Arg Thr																
1 5																
ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa															163	
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu																
10 15 20																
atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat															211	
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp																
25 30 35																
ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac															259	
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His																
40 45 50																
gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca															307	
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala																
55 60 65																
cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg															355	
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp																
70 75 80 85																
cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc															403	
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly																
90 95 100																
acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac															451	
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His																
105 110 115																
ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc															499	
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe																
120 125 130																
cct aac ctg taatttttac ggtagaaaa aaa															531	
Pro Asn Leu																
135																

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<210> 994
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<212> PRT
<213> Corynebacterium glutamicum
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<400> 994
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Gly His Val	Gly Glu Ile Ile	Ala Arg Ile Glu Arg	Lys Gly Leu Lys
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Leu Ala Ala	Leu Asp Leu Arg	Val Ala Asp Arg	Glu Thr Ala Glu Lys
	35	40	45
His Tyr Glu	Glu His Ala Asp	Lys Pro Phe Phe	Gly Glu Leu Val Glu
	50	55	60
Phe Ile Thr	Ser Ala Pro Leu	Ile Ala Gly Ile	Val Glu Gly Glu Arg
	65	70	75
Ala Ile Asp	Ala Trp Arg Gln	Leu Ala Gly Gly	Thr Asp Pro Val Ala
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile	Arg Gly Asp Phe	Ala Leu Thr Val Gly
	100	105	110
Glu Asn Val	Val His Gly Ser	Asp Ser Pro Glu	Ser Ala Glu Arg Glu
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Ile Ser Ile	Trp Phe Pro Asn	Leu	
	130	135	

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<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(808)

<223> RXA00718

<400> 995

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actcctctga gctgaccagc ttatacaagg tgggtccaact gtg acg gaa att tcc 115
                               Val Thr Glu Ile Ser
                               1                               5

aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
                               10                               15                               20

acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
                               25                               30                               35

aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
                               40                               45                               50

ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
                               55                               60                               65

acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

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Thr	Ala	Val	Leu	Pro	Leu	Ser	Ile	Ser	Asp	Asp	Pro	Ala	Ser	Thr	Glu	
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gtg	ttg	ctc	gcg	ggc	gtc	gat	gtg	caa	aag	gac	atc	cgc	gga	cca	gaa	403
Val	Leu	Leu	Ala	Gly	Val	Asp	Val	Gln	Lys	Asp	Ile	Arg	Gly	Pro	Glu	
				90					95					100		
gtc	acc	caa	aat	gtc	tcc	gca	gtg	tcc	gcg	atc	cct	gag	gtt	cgt	gaa	451
Val	Thr	Gln	Asn	Val	Ser	Ala	Val	Ser	Ala	Ile	Pro	Glu	Val	Arg	Glu	
			105					110						115		
aac	ttg	gtg	gcg	ttg	cag	cgc	gca	ctc	gcc	gcc	aaa	gca	cat	cgc	tgc	499
Asn	Leu	Val	Ala	Leu	Gln	Arg	Ala	Leu	Ala	Ala	Lys	Ala	His	Arg	Cys	
			120				125						130			
gtc	gtc	gaa	ggc	aga	gac	atc	gga	acg	gca	gtg	ctt	gtc	gac	gcg	ccc	547
Val	Val	Glu	Gly	Arg	Asp	Ile	Gly	Thr	Ala	Val	Leu	Val	Asp	Ala	Pro	
			135				140									
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Ile	Lys	Ala	Phe	Leu	Thr	Ala	Ser	Ala	Glu	Val	Arg	Ala	Gln	Arg	Arg	
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ttt	gac	caa	gac	acc	gca	gca	ggc	cgc	gac	gta	gat	ttc	gac	gct	gtg	643
Phe	Asp	Gln	Asp	Thr	Ala	Ala	Gly	Arg	Asp	Val	Asp	Phe	Asp	Ala	Val	
				170					175						180	
ctg	gca	gat	gtt	gtt	cgc	cgc	gat	gaa	cta	gat	tcc	acc	cgt	gcc	gcc	691
Leu	Ala	Asp	Val	Val	Arg	Arg	Asp	Glu	Leu	Asp	Ser	Thr	Arg	Ala	Ala	
				185				190						195		
tca	ccg	ctg	aaa	cca	gca	gat	gat	gca	cac	atc	gtg	gac	acc	tct	gat	739
Ser	Pro	Leu	Lys	Pro	Ala	Asp	Asp	Ala	His	Ile	Val	Asp	Thr	Ser	Asp	
			200				205						210			
atg	acc	atg	gat	caa	gta	ctt	gat	cac	ctc	atc	cac	cta	gtg	gaa	gcc	787
Met	Thr	Met	Asp	Gln	Val	Leu	Asp	His	Leu	Ile	His	Leu	Val	Glu	Ala	
			215			220					225					
tcc	gct	gaa	agg	agc	aac	cag	tgactgataa	acacacccatg	cct							831
Ser	Ala	Glu	Arg	Ser	Asn	Gln										
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<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 996

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Asp	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Ser	Thr	Thr	Ser	Arg	Ala	Leu	Ala	
			20					25					30			
Thr	Arg	Leu	Ser	Ala	Lys	Tyr	Leu	Asp	Thr	Gly	Ala	Met	Tyr	Arg	Val	
		35					40					45				
Ala	Thr	Leu	His	Val	Leu	Asn	Gln	Gly	Ile	Asp	Pro	Ala	Asp	Ser	Ala	
		50				55					60					

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile
210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln
225 230 235

<210> 997

<211> 1785

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1762)

<223> RXA01599

<400> 997

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tcgatgttta ggttcaacca ggaaggctgt ctcagacatc atg acc tct agt cga 115
Met Thr Ser Ser Arg
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
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gtt	gat	ccg	ggc	acc	atg	aat	cct	ttt	gaa	cac	ggg	gaa	gtc	ttt	gtc	307
Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
		55				60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
		70			75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90				95						100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110					115			
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
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Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
		135				140					145					
gtg	atc	tct	gag	gtc	ggg	ggc	acc	gtc	ggg	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
					155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggg	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
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tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggg	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggg	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
		215				220					225					
cct	caa	ggg	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
					235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265				270						275			
ggc	ctt	ccg	ttc	cgt	gat	gtt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

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gaa cgg gtg aac aac cca cgc cat gag ctc acc gtc ggc atc gtg ggc		
1027		
Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly		
295	300	305
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt		
1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val		
310	315	320 325
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att		
1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile		
	330	335 340
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc		
1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser		
	345	350 355
ggg ttg gat gcc atc gtg gtt ccc gga ggt ttc ggt atc cga ggt atc		
1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile		
	360	365 370
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg		
1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro		
	375	380 385
ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca		
1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala		
390	395	400 405
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct		
1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala		
	410	415 420
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg		
1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val		
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tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct		
1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro		
	440	445 450
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg		
1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr		
	455	460 465
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac		
1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr		
470	475	480 485

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu
535 540 545

ctg cgt gtc cac cct tagatctaca atgtgatcat ggt
1785

Leu Arg Val His Pro
550

<210> 998

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 998

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20 25 30

Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145		150		155		160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
		165		170		175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
		180		185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
		195		200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
		210		215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
		225		230		235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
		245		250		255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
		260		265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
		275		280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
		290		295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
		305		310		315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
		325		330		335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
		340		345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
		355		360		365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
		370		375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
		385		390		395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
		405		410		415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
		420		425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
		435		440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
		450		455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
		465		470		475
						480



Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val
 485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr
 500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu
 515 520 525

Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val
 530 535 540

Lys Thr Ala Leu Glu Leu Arg Val His Pro
 545 550

<210> 999

<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3439)

<223> RXN02234

<400> 999

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tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115
 Met Pro Lys Arg Ser
 1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
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cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
 Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
 25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259
 Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
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atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307
 Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
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 Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly
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cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
 90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451
 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
 105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499
 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp
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cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala
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cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595
 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala
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 Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly
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ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691
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 200 205 210

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr
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gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835
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 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu
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act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile
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 295 300 305

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 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
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 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
 390 395 400 405

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 1363
 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
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 1891
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 1939
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
 600 605 610

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 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
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 2179
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
 680 685 690

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 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
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 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
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 2995
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 3043
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 970 975 980

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 3091
 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
 985 990 995

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 3139
 Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
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 3235
 Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
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 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
 1050 1055 1060

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 Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu
 1065 1070 1075

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 3379
 Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
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 3427
 Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His
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 Ala Val Lys Ala
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Pro	Ile	Val	Ile	Gly	Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	20	25	30	
Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	35	40	45	
Ser	Asn	Pro	Ala	Thr	Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	50	55	60	
Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys	65	70	75	80
Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	85	90	95	
Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	100	105	110	
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	115	120	125	
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	130	135	140	
Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	145	150	155	160
His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	165	170	175	
Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	180	185	190	
Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	195	200	205	
Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	210	215	220	
Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	225	230	235	240
Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	245	250	255	
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln				

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Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn
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Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu
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Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr
				325					330					335	
Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe
			340					345					350		
Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe
		355					360					365			
Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser
	370					375					380				
Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn
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Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys
				405					410					415	
Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val
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Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu
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Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala	Ser
	450					455					460				
Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe
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Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg
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Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu	Arg
			500					505					510		
Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser	Leu
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Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu	Phe
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Ala	Glu	Ser	Glu	Val	Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu	Ile
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Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr
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Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
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 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
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 740 745 750
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 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys
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 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu
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 Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg
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 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala
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 965 970 975
 Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile
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 1056
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 1824
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 595 600 605
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 1872
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 1920
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 625 630 635 640
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 1968
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 2016
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
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675	680	685
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gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg 2208		
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
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Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		



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 885 890 895

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 915 920 925

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 2832
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940

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 2880
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960

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aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
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 980 985 990

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 995 1000 1005

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 3072
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 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055

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<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

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Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
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Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
		195					200					205			
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
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Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
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Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
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Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
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 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
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 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
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 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
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 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
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 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
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 485 490 495
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
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 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
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625					630					635					640
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
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Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
			660					665					670		
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	690					695					700				
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Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu
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Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu
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785					790					795					800
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	850					855					860				
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865					870					875					880
Arg	Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys
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			900					905					910		
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Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
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Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
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Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
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Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
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Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
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Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
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<223> RXN00450

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 Val Gly Val Leu Pro
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gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
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 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
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 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
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 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
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gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

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<211> 108

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Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
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Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
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 Val Gly Val Leu Pro
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Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
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Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
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gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
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Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
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Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
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Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
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                                         Val Arg Ile Thr Asn
                                         1      5

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Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                      55                      60                      65

cct  cgc  gaa  aac  tct  tcc  ggc  aca  ctt  ttt  gaa  gcc  atc  gaa  atc  tgg      355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
                      70                      75                      80                      85

gcc  gac  cgc  aag  acc  caa  ggc  ttc  cac  atc  aaa  gaa  gac  att  aaa  gcg      403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
                      90                      95                      100

aag  gcc  ctc  cag  gca  gcc  cgt  cgg  gca  gca  gaa  cac  ggc  gtt  ggt  ttc      451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
                      105                      110                      115

atc  cgc  act  cac  gta  gat  gtc  acc  gat  ccc  acg  ttt  gct  gga  ttc  gaa      499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
                      120                      125                      130

gca  att  gcg  gag  ctg  cgc  gat  gaa  gtc  cgc  gag  tgg  tgc  gat  atc  cag      547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
                      135                      140                      145

att  gtc  gcc  ttc  ccg  caa  aat  ggc  att  tac  gcc  tac  gaa  ggt  ggc  cag      595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
                      150                      155                      160                      165

aag  cta  atc  tca  gat  gca  atg  tct  gca  ggt  gca  gat  gtc  gtt  ggt  ggc      643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
                      170                      175                      180

atc  cca  cac  ctt  gaa  ccc  acc  cga  gac  gat  ggc  gtc  gag  tcg  gtg  aaa      691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
                      185                      190                      195

tgg  ctg  ttc  gac  ctt  gca  gag  aag  cac  tca  gcc  ccc  atc  gat  atc  cac      739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His
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200	205	210	
act gat gaa att gac gat	cca cat tcc cga ttt gtc	gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp	Pro His Ser Arg Phe Val	Glu Val Leu Ala	
215	220	225	
gca gaa gcc gca aaa cgt gac atg ggc gca	caa acc gtg gtg tct cat		835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala	Gln Thr Val Val Ser His		
230	235	240	245
tct gtg gcg atg gcc tat tac tca cct ggc	tac atg gcg cga ctt tta		883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly	Tyr Met Ala Arg Leu Leu		
250	255	260	
ccc aag ctc gca gca tca aag gtt cgt ttt	gca gta tgc ccc aat gaa		931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe	Ala Val Cys Pro Asn Glu		
265	270	275	
aac ctc cat ctg caa gga ctt ggt ttc caa	gga ccc gtc ccc cga ggt		979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln	Gly Pro Val Pro Arg Gly		
280	285	290	
gtt gca ccg gta aag caa ctt acc gaa tgg	gga att cca gta agt ttt		
1027			
Val Ala Pro Val Lys Gln Leu Thr Glu Trp	Gly Ile Pro Val Ser Phe		
295	300	305	
tgc cag gac tca ctc aat gac ccc ttc tac	ccc atg ggc gat gga gat		
1075			
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr	Pro Met Gly Asp Gly Asp		
310	315	320	325
cta ctc cgc att ctc gat tct gga tta cac	gtg tcc cac atg ctc aca		
1123			
Leu Leu Arg Ile Leu Asp Ser Gly Leu His	Val Ser His Met Leu Thr		
330	335	340	
gcc agc cac ttg aag aat gca cta tcg ttc	atc acc acc aat cca gcc		
1171			
Ala Ser His Leu Lys Asn Ala Leu Ser Phe	Ile Thr Thr Asn Pro Ala		
345	350	355	
gga aac cta ggc ctg gac aat tac gac att	gca gaa aac tcc ccg gcg		
1219			
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile	Ala Glu Asn Ser Pro Ala		
360	365	370	
aac ctg ctg gtt ctt gat gcg agc agc gag	aag gaa gct gta cag aga		
1267			
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu	Lys Glu Ala Val Gln Arg		
375	380	385	
aaa gct tcc gta ctt ttg agc atc cac cgc	ggc aaa aag gtg ctc tcc		
1315			
Lys Ala Ser Val Leu Leu Ser Ile His Arg	Gly Lys Lys Val Leu Ser		
390	395	400	405
agg gag ccc gaa cag gtg gac tgg aac atc	taacagccca gttgggcctc		
1365			
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile			
410	415		

ctt
1368

<210> 1008

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1008

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20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
 405 410 415

<210> 1009

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA02272

<400> 1009

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 Val Arg Ile Thr Asn
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
 Glu Lys Ile Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
 55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	
1027	
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
390 395 400 405

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1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
410 415

ctt
1368

<210> 1010

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

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20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405

410

415

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(580)
 <223> RXN03004

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 Val Leu Leu Ser Asp
 1 5
 cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163
 Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro
 10 15 20
 ttc gac gct gag ctg att cag ccg tcg agt gtc gat gtc cgc atg gac 211
 Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp
 25 30 35
 cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259
 Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro
 40 45 50
 aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307
 Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly
 55 60 65
 gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355
 Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
 70 75 80 85
 gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
 90 95 100
 tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
 105 110 115
 att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
 120 125 130
 gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
 135 140 145
 gct ttg ttc cag atg agt tcc cct gcg gag act 580
 Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
 150 155 160

<210> 1012
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1012
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 Leu Gly Ile Glu Pro Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val
 20 25 30
 Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr
 35 40 45
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val
 50 55 60
 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val
 65 70 75 80
 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly
 85 90 95
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His
 100 105 110
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu
 115 120 125
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met
 130 135 140
 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
 145 150 155 160

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(202)
 <223> RXN03137

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 Leu Glu Leu Asn Lys
 1 5
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly
 10 15 20

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcggtgc 212
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val
 25 30

gatttgggca caa 225

<210> 1014

<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

Leu Glu Leu Asn Lys Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp
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Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val
 20 25 30

Ala Val

<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1015

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cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt gcc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1016

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1016

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 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser

165

170

<210> 1017
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> FRXA02857

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 Met Asp Ile Thr Ile
 1 5
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100
 cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
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<213> Corynebacterium glutamicum

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20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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Val Ser Glu Gln Ala
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
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tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
 25 30 35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
 40 45 50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
 90 95 100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 150 155 160 165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
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 Arg Asp Pro Gln
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tgattgacac ctgaatctac aacacaaggg gaacgcgcacg atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
10 15 20

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307

Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu
 55 60 65
 gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355
 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met
 70 75 80 85
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg
 90 95 100
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile
 105 110 115
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg
 120 125 130
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu
 135 140 145
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly
 150 155 160 165
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala
 170 175 180
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691
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 Tyr Ser Asp
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<213> Corynebacterium glutamicum

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 35 40 45
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly
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Glu	Ile	Leu	Thr	Tyr	Glu	Met	Phe	Gly	Thr	Ala	Met	Arg	Glu	Leu	Ala
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Arg	Gly	Gly	Leu	Leu	Ile	Gly	Gly	Ala	Leu	Gly	Tyr	Ala	Leu	Gly	Ile
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aag aat gta tcg gtg atc aat gtg gag ttc tac acc gat att gga gag															307
Lys	Asn	Val	Ser	Val	Ile	Asn	Val	Glu	Phe	Tyr	Thr	Asp	Ile	Gly	Glu
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His	Leu	Glu	Glu	Pro	Met	Met	Leu	Pro	Pro	Thr	Pro	Lys	Ala	Val	Asp
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ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
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 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
 105 110 115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
 120 125 130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
 135 140 145

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<213> Corynebacterium glutamicum

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 35 40 45

Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr
 50 55 60

Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
 65 70 75 80

Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
 85 90 95

Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
 100 105 110

Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
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Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
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 Met Ser Glu Asn Leu
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cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag 163
 Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
 10 15 20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc 211
 Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
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att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc 259
 Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
 40 45 50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag 307
 Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
 55 60 65

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc 355
 Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
 70 75 80 85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403
 Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
 90 95 100

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 Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
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acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499
 Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
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aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547
 Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
 135 140 145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595
 Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
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 Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
 170 175 180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
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<210> 1026

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
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Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
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Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
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Val Thr
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 <223> RXN02772

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Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
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Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
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att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
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Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
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Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
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Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
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cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
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aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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 200 205 210

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
 215 220 225

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 Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys
 295 300 305

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 20 25 30

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Pro	Leu	Ala	Val	Ala	Thr	Ile	Ala	Ala	Glu	Ile	Gly	Met	Asp	Thr	Thr
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Thr	Leu	Val	Ala	Ala	Leu	Leu	His	Asp	Thr	Val	Glu	Asp	Thr	Asp	Tyr
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Lys	Trp	Glu	Leu	Glu	Asp	Leu	Ser	Phe	Ala	Ile	Leu	Tyr	Pro	Lys	Lys
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Ile	Gln	Arg	Leu	Tyr	Phe	Ser	Pro	Ala	Leu	Arg	Cys	Leu	Pro	Ile	Pro
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 230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
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<213> Corynebacterium glutamicum

<400> 1030

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 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 50 55 60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
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Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 85 90 95

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 100 105 110

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
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Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
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Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 180 185 190
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 195 200 205
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 210 215 220
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
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 Met Ile Val Arg Gly
 1 5
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa
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 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
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 Leu

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Met Asn Thr Ala Ala
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Trp	Ala	His	Arg	His	His	Val	Arg	Lys	Gly	Gly	Gly	Ile	Pro	Tyr	Val	
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agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
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gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
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ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
70 75 80 85

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Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
          90                      95                      100

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Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
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 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
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 Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
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 Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
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 Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
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 Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
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 Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
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 Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
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 Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
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 <213> Corynebacterium glutamicum

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<222> (101)..(1372)

<223> RXA01483

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Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
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gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
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caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
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cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
                               70                               75                               80                               85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
                               90                               95                               100

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Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
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                               120                               125                               130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
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Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
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tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
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Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg	
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Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala	
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Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu	
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Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Asp	
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Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser	
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Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys	
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1315	
Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr	
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<211> 424

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1036

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 Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45
 Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
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 Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80
 Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95
 Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
 100 105 110
 Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125
 Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140
 Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160
 Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
 165 170 175
 Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190
 Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
 195 200 205
 Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
 210 215 220
 Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
 225 230 235 240
 Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro



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Ala Ala Ala Ala Asp Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu																		
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Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile																		
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Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu						325				330						335		
Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala								345					350					
Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu							360					365						
Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe							375				380							
Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln						390				395							400	
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Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile																		
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Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp	
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Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro	
70 75 80 85	
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Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg	
90 95 100	
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Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr	
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Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala	
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Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg	
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Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro	
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Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp	
215 220 225	
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Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp	
230 235 240 245	
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Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro	
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Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val	
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Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
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 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
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Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
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Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
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Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
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Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
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Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
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Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
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Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
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Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
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Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
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Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
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<212> DNA

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<220>

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<222> (101)..(757)

<223> FRXA01024

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aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
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cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

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Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
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gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
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aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
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aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
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tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
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gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
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<211> 219

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<400> 1040

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Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
		35					40					45			

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
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 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys
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<210> 1041

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(234)

<223> FRXA01027

<400> 1041

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 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30
 atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45
 aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

taggagcgcg tttaaggcct cca 257

<210> 1042

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

<210> 1043

<211> 651

<212> DNA

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<220>

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<222> (101)..(628)

<223> RXA01528

<400> 1043

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gggtcgtagg tctccaacca ggaggcgttc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

55 60 65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
 Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
 70 75 80 85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
 Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
 90 95 100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
 Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
 105 110 115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
 Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
 120 125 130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
 Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
 135 140 145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
 Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
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aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648
 Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
 170 175

aac 651

<210> 1044
 <211> 176
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1044
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 Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
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 35 40 45
 Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
 50 55 60
 Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
 65 70 75 80
 Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
 85 90 95
 Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
 100 105 110
 His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu 130 135 140		
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu 145 150 155 160		
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg 165 170 175		
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<212> DNA		
<213> Corynebacterium glutamicum		
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	Met Ser Phe Gln Leu	5
	1	
ggt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163		
Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser		20
	10 15	
ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211		
Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys		35
	25 30	
cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259		
His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala		50
	40 45	
agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307		
Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala		65
	55 60	
att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355		
Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala		85
	70 75 80	
gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403		
Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr		100
	90 95	
cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451		
His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr		115
	105 110	
tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499		

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
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 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala
 135 140 145

<210> 1046
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1046
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 Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser
 20 25 30
 Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala
 35 40 45
 Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60
 His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80
 Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95
 Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110
 Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125
 Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
 130 135 140
 Asn Pro Ala
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<210> 1047
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(979)
 <223> RXA01878

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 atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115
 Met Glu Glu Pro Ser
 1 5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag	163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys	
10 15 20	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat	211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp	
25 30 35	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac	259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn	
40 45 50	
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc	307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala	
55 60 65	
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt	355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg	
70 75 80 85	
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt	403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu	
90 95 100	
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa	451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln	
105 110 115	
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac	499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr	
120 125 130	
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc	547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr	
135 140 145	
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg	595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu	
150 155 160 165	
gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg	643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala	
170 175 180	
tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc	691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val	
185 190 195	
ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc	739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg	
200 205 210	
gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg	787
Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp	
215 220 225	
ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct	835
Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala	
230 235 240 245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys
 280 285 290

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 1002

<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln
 20 25 30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala
 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
 275 280 285

Gln Lys Asp Glu Lys
 290

<210> 1049
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1531)
 <223> RXN02281

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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451

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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
		120					125					130					
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547	
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp		
		135				140						145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	cgc	595	
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
150					155					160					165		
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643	
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile		
				170					175					180			
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691	
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
			185				190						195				
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739	
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met		
		200					205						210				
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggt	cta	tcc	ttg	cca	787	
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
		215				220					225						
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggt	acg	gaa	835	
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
230					235					240					245		
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883	
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
				250					255					260			
acc	gaa	gcc	ggt	gac	ggt	att	acc	att	atc	aac	atc	ggt	gtg	ggc	cca	931	
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
			265				270						275				
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
		280					285					290					
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc		
1027																	
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
		295				300					305						
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1075																	
Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile		
310					315					320					325		
ctg	aat	acc	cgc	atc	cca	ctt	ggt	aat	ccg	atc	ccg	gca	ata	cca	gaa		
1123																	
Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile	Pro	Ala	Ile	Pro	Glu		
				330					335					340			

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
410 415 420

cca cta cac gca gtg cgc aaa ctt tcc gcg caa gcg cag gcg ttt tac
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
455 460 465

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1545

Thr Leu Gly Glu Val Pro Phe Arg
470 475

<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
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Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
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 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
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<211> 1191

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1168)

<223> FRXA02281

<400> 1051

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 Val Gln Lys Asp Ser 5
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 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu 20
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn 35
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 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr 50
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 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly 65
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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg 85
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 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

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Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro					
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1123

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atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

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<211> 356

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<213> Corynebacterium glutamicum

<400> 1052

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
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Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
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 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
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 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
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 <223> RXN01240

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 Met Ser Asp Asn Thr
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 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro
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 25 30 35
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 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
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Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
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Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
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Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu	
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Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His	
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Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser	
170 175 180	
gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta	691
Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu	
185 190 195	
gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga	739
Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg	
200 205 210	
gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt	787
Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac	835
Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
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Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
250 255 260	
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Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu	
265 270 275	
aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
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Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val	
295 300 305	

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac
1123

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<211> 341

<212> PRT

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<400> 1054

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35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
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Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

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Pro Arg Ser Thr	Asn Tyr Arg Phe Leu Glu Asp	Ile Leu Val Ala Asn
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Ser Ile Thr Ser	Val Val Gln Leu Arg Glu Leu Leu	Asn Pro Thr Asp
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Ile Glu Val Leu Leu Lys	Val Met Asn Tyr Arg Phe	His Pro Gly Gln
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Ile Arg Ile Ile Asp	Asp Leu Leu Leu Lys Arg	Phe Gly Gln Ser His
	290	295 300
Ile Asp Ala Thr Val	Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg	
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1234)

<223> RXN02008

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Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
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Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
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gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259
Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
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gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
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 Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys
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 Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala
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 180 185 190
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys
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 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala
 210 215 220
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser
 225 230 235 240
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala
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 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val
 260 265 270
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala
 275 280 285
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 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met
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 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe
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<212> DNA

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<223> RXN01940

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 Met Thr Thr Lys Ile
 1 5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc	163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
10 15 20	
gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc	211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc	259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
40 45 50	
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca	307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
55 60 65	
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc	355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
70 75 80 85	
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa	403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
90 95 100	
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag	451
Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu	
105 110 115	
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg	499
Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala	
120 125 130	
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt	547
Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val	
135 140 145	
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct	595
Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala	
150 155 160 165	
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac	643
Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn	
170 175 180	
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg	691
Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
185 190 195	
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac	739
Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp	
200 205 210	
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac	787
Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr	
215 220 225	
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct	835
Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala	
230 235 240 245	
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260
 ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275
 gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290
 gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag
 1027
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys
 295 300 305
 cgc atc gga tagacctgtt cacaagggttg tta
 1059
 Arg Ile Gly
 310
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 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1058
 Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala
 1 5 10 15
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly
 20 25 30
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn
 35 40 45
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
 50 55 60
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
 65 70 75 80
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
 85 90 95
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
 100 105 110
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
 115 120 125
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
 130 135 140
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
 145 150 155 160
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
 165 170 175



His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
 180 185 190
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
 195 200 205
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
 210 215 220
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
 225 230 235 240
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
 245 250 255
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
 260 265 270
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
 275 280 285
 Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val
 290 295 300
 Ile Asp Ala Val Lys Arg Ile Gly
 305 310

<210> 1059
 <211> 602
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(579)
 <223> FRXA01940

<400> 1059
 aga gta acg ctt gtt tcc acc ggg cca ctg acc aac atc gcg ctg gca 48
 Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala
 1 5 10 15
 gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96
 Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu
 20 25 30
 atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144
 Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe
 35 40 45
 aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192
 Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
 50 55 60
 tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240
 Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
 65 70 75 80
 aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc 288
 Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala

	85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac				336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp				
	100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca				384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala				
	115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat				432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp				
	130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc				480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe				
	145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg				528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu				
	165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc				576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile				
	180	185	190	
gga tagacctgtt cacaagggtg tta				602
Gly				

<210> 1060

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 1060

Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala				
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Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu				
20	25	30		
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe				
35	40	45		
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys				
50	55	60		
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala				
65	70	75	80	
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala				
85	90	95		
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp				
100	105	110		
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala				
115	120	125		

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
 130 135 140
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
 145 150 155 160
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
 165 170 175
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
 180 185 190

Gly

<210> 1061
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1003)
 <223> RXA02559

<400> 1061
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 aaccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115
 Met Ile Pro Val Leu
 1 5
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
 10 15 20
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
 25 30 35
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp
 40 45 50
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
 55 60 65
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
 70 75 80 85
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
 90 95 100
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787
Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
215 220 225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
230 235 240 245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
250 255 260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
265 270 275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
280 285 290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cggtgctgat gca
1026
Ala Glu Leu Leu Arg Ala Val Glu
295 300

<210> 1062

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1062

Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu
1 5 10 15

Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu
20 25 30



Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
 35 40 45
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
 50 55 60
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
 65 70 75 80
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
 85 90 95
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
 100 105 110
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
 115 120 125
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
 130 135 140
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val
 145 150 155 160
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile
 165 170 175
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp
 180 185 190
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu
 195 200 205
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln
 210 215 220
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile
 225 230 235 240
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val
 245 250 255
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg
 260 265 270
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp
 275 280 285
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu
 290 295 300

<210> 1063

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 1063

tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag
 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacatttac ccggaagga gtt
 1050

<210> 1064

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285
 Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300
 Asp Lys Gly Leu Glu
 305

<210> 1065
 <211> 2226
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(2203)
 <223> RXN01079

<400> 1065
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 Met Asp Phe His Ala
 1 5
 ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20
 gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35
 cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
ggt	gaa	aac	aag	tac	tat	gac	cca	atc	ggt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60				65						
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
	70				75					80					85	
ttc	cag	tcc	ttc	ctc	ggt	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90					95					100		
aag	acc	ttc	gac	ggt	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
			105					110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
	150				155				160						165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggt	ggc	gta	gcg	ttg	ctg	691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190					195			
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggt	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205					210				
cag	tct	tcc	ggt	ggt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc	tac	gct	aac	cag	ctg	ggt	gct	cgt	cag	ggt	gca	ggt	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
	230				235				240					245		
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
				250				255						260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggt	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
		265					270						275			
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	

280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr
505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr
665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt
 2179
 Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val
 680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc
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 Asp Gly Cys Val Ser Cys Met Leu
 695 700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

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Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly
 225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe
 245 250 255
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr
 260 265 270
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys
 275 280 285
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile
 290 295 300
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu
 305 310 315 320
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln
 325 330 335
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr
 340 345 350
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg
 355 360 365
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro
 370 375 380
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile
 385 390 395 400
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro
 405 410 415
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val
 420 425 430
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn
 435 440 445
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr
 450 455 460
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe
 465 470 475 480
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser
 485 490 495
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn
 500 505 510
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp
 515 520 525
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn
 530 535 540
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val
 545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr
565 570 575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile
580 585 590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr
595 600 605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp
610 615 620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala
625 630 635 640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp
645 650 655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg
660 665 670

Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu
675 680 685

Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
690 695 700

<210> 1067

<211> 790

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> FRXA01079

<400> 1067

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gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115
Met Asp Phe His Ala
1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259
Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu
40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe
55 60 65

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cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
70 75 80 85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu
90 95 100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
105 110 115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
120 125 130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
135 140 145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys
150 155 160 165

ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile
170 175 180

aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu
185 190 195

ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile
200 205 210

cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe
215 220 225

tcc 790
Ser
230

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<210> 1068

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1068

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Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
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Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

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50 55 60
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220
 Leu Glu Asp Ala Phe Ser
 225 230

<210> 1069

<211> 1364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1341)

<223> FRXA01084

<400> 1069

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 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
 1 5 10 15

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg 96
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag 144
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45

cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac 192
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg 240			
Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 80			
65 70		75	
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac 288			
Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 95			
85 90			
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa 336			
Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 110			
100 105		110	
ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc 384			
Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 125			
115 120		125	
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa 432			
Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 140			
130 135		140	
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat 480			
Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 160			
145 150		155	
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act 528			
Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 175			
165 170		175	
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag 576			
Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 190			
180 185		190	
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac 624			
Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 205			
195 200		205	
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg 672			
Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 220			
210 215		220	
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt 720			
Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 240			
225 230		235	
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc 768			
Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 255			
245 250		255	
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca 816			
Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 270			
260 265		270	
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag 864			
Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 285			
275 280		285	
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc 912			
Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 300			
290 295		300	

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac
 1008
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc
 1056
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc
 1104
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct
 1152
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc
 1200
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca
 1248
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt
 1296
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg
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 435 440 445

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<210> 1070

<211> 447

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1070

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Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe



355				360				365							
Glu	Asp	Ala	Tyr	Glu	Ile	Gly	Tyr	Glu	Lys	Ile	Ile	Asp	Thr	Tyr	Ala
	370					375					380				
Val	Ala	Thr	Lys	Tyr	Val	Asp	Gln	Gly	Leu	Ser	Leu	Thr	Leu	Phe	Phe
385					390					395					400
Lys	Asp	Thr	Ala	Thr	Thr	Arg	Asp	Ile	Asn	Arg	Ala	Gln	Ile	Tyr	Ala
				405					410					415	
Trp	Arg	Lys	Gly	Ile	Lys	Thr	Leu	Tyr	Tyr	Ile	Arg	Leu	Arg	Gln	Val
			420					425					430		
Ala	Leu	Glu	Gly	Thr	Glu	Val	Asp	Gly	Cys	Val	Ser	Cys	Met	Leu	
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<211> 1125
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1102)  
<223> RXN01920
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																Met	Ala	Ala	Asp	Ser	
																1				5	
gat	ctc	agt	gtt	cac	gat	gct	tac	tta	aag	gag	cat	gtt	gca	cct	gta	163					
Asp	Leu	Ser	Val	His	Asp	Ala	Tyr	Leu	Lys	Glu	His	Val	Ala	Pro	Val						
				10					15					20							
aag	gcg	atc	aac	tgg	aac	tcc	atc	cca	gat	tcc	aaa	gat	ctt	gaa	gtc	211					
Lys	Ala	Ile	Asn	Trp	Asn	Ser	Ile	Pro	Asp	Ser	Lys	Asp	Leu	Glu	Val						
				25					30					35							
tgg	gat	cgt	ctg	acc	ggg	aac	ttc	tgg	ctc	cca	gaa	aag	gtc	cca	gta	259					
Trp	Asp	Arg	Leu	Thr	Gly	Asn	Phe	Trp	Leu	Pro	Glu	Lys	Val	Pro	Val						
				40					45					50							
tcc	aac	gac	atc	aag	agc	tgg	gga	acc	ctc	aac	gag	gtt	gaa	aaa	gcc	307					
Ser	Asn	Asp	Ile	Lys	Ser	Trp	Gly	Thr	Leu	Asn	Glu	Val	Glu	Lys	Ala						
				55					60					65							
gca	acc	atg	cgc	gtg	ttc	acc	gga	ctt	acc	ctg	ctg	gac	acc	att	cag	355					
Ala	Thr	Met	Arg	Val	Phe	Thr	Gly	Leu	Thr	Leu	Leu	Asp	Thr	Ile	Gln						
				70					75					80	85						
ggc	act	gtc	ggc	gca	atc	tcc	ctg	ctt	cca	gac	gca	gat	tca	ctg	cac	403					
Gly	Thr	Val	Gly	Ala	Ile	Ser	Leu	Leu	Pro	Asp	Ala	Asp	Ser	Leu	His						
				90					95					100							
gaa	gaa	gcg	gtg	cta	acc	aac	att	gcg	ttc	atg	gaa	tcc	gtg	cac	gca	451					
Glu	Glu	Ala	Val	Leu	Thr	Asn	Ile	Ala	Phe	Met	Glu	Ser	Val	His	Ala						

105	110	115	
aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc			499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile			
120	125	130	
aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag			547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys			
135	140	145	
gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc			595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg			
150	155	160	165
aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc ggc ttc			643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe			
170	175	180	
tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc			691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala			
185	190	195	
gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac tac			739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr			
200	205	210	
att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt			787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg			
215	220	225	
cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac			835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr			
230	235	240	245
gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg			883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp			
250	255	260	
acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc			931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu			
265	270	275	
aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag gtg			979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val			
280	285	290	
tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac			
1027			
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His			
295	300	305	
gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa			
1075			
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu			
310	315	320	325
aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag			
1122			
Asn Thr Glu Asp Asp Asp Trp Asp Phe			
330			



cgc
1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu
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His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser
20 25 30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro
35 40 45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn
50 55 60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu
65 70 75 80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp
85 90 95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met
100 105 110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala
115 120 125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu
130 135 140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp
145 150 155 160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu
165 170 175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys
180 185 190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala
195 200 205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys
210 215 220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu
225 230 235 240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr
245 250 255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn
260 265 270



Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala
 275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn
 290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 325 330

<210> 1073
 <211> 437
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(414)
 <223> FRXA01920

<400> 1073
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 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
 1 5 10 15

tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

cgc 437

<210> 1074
 <211> 138
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1074
 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
 1 5 10 15
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

<210> 1075
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(544)
 <223> RXA01080

<400> 1075
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 ttgcgcacaa acggtattta gaaggggaagt gagttcgagg atg cta atc gtg tat 115
 Met Leu Ile Val Tyr
 1 5
 ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
 10 15 20
 tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
 25 30 35


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atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
      40                      45                      50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg
      55                      60                      65

ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
      70                      75                      80                      85

ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
      90                      95                      100

att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
      105                      110                      115

ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
      120                      125                      130

gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
      135                      140                      145

taaaccttaa aacttaatca atc 567

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<210> 1076

<211> 148

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1076

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  1                      5                      10                      15

Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
      20                      25                      30

Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
      35                      40                      45

Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
      50                      55                      60

Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
      65                      70                      75                      80

Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
      85                      90                      95

Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
      100                      105                      110

Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
      115                      120                      125

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Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro
 130 135 140

Val Thr Ser Arg
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<210> 1077

<211> 650

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	



gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg 650
 Asp

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
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Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

<210> 1079
 <211> 630
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(630)
 <223> RXA01416

<400> 1079
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 Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
 1 5 10 15
 gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca 96
 Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30
 ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt 144
 Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45
 gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag 192
 Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60
 gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg 240
 Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80
 ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac 288
 Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95
 atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac 336
 Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110
 agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct 384
 Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125
 gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc 432
 Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140
 atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt 480
 Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160
 gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag 528
 Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175
 acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag 576
 Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

tac aac 630
 Tyr Asn
 210

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
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Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

Tyr Asn
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<210> 1081

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA01486

<400> 1081

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Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

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gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
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acc ttc tcc gac gtc gca 757
 Thr Phe Ser Asp Val Ala
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<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

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 20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
 35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
 50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
 65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
 85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
 100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
 115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
 130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
 145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
 165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
 180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
 195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
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<210> 1083

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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              Met Leu Lys Cys Ala
              1                      5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
              10                      15                      20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
              25                      30                      35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
              40                      45                      50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
              55                      60                      65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
              70                      75                      80                      85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
              90                      95                      100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
              105                      110                      115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
              120                      125                      130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
              135                      140                      145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
              150                      155                      160                      165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagttcgtg atctaggaac 648
Asn Ile Asp Val Val Phe Ala Gly His Thr His
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cga 651

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<210> 1084
 <211> 176
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1084
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 20 25 30
 Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
 35 40 45
 Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
 50 55 60
 Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
 65 70 75 80
 Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
 85 90 95
 Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
 100 105 110
 Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
 115 120 125
 Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
 130 135 140
 Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
 145 150 155 160
 Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
 165 170 175

<210> 1085
 <211> 1359
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1336)
 <223> RXA01679

<400> 1085
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 Met Gln Ser Gly Asn
 1 5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggg gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly
 250 255 260
 caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu
 265 270 275
 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
 280 285 290
 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca
 1027
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
 295 300 305
 att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg
 1075
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
 310 315 320 325
 aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc
 1123
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
 330 335 340
 gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att
 1171
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
 345 350 355
 gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta
 1219
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
 360 365 370
 gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta
 1267
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
 375 380 385
 gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag
 1315
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
 390 395 400 405
 atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat
 1359
 Ile Gln Gln Gln Ile Phe Ala
 410

<210> 1086

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser
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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu
 20 25 30
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala
 35 40 45
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
 65 70 75 80
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
 85 90 95
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
 100 105 110
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
 115 120 125
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
 145 150 155 160
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
 165 170 175
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
 180 185 190
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
 195 200 205
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
 305 310 315 320
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
 325 330 335
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser



340	345	350	
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala			
355	360	365	
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile			
370	375	380	
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro			
385	390	395	400
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala			
405	410		
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<212> DNA			
<213> Corynebacterium glutamicum			
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<221> CDS			
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<223> RXN01488			
<400> 1087			
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gccccgacctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc 115			
		Met Ser Lys Lys Ala	
		1 5	
atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163			
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr			
10 15 20			
gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211			
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr			
25 30 35			
ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259			
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu			
40 45 50			
gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307			
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His			
55 60 65			
gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355			
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile			
70 75 80 85			
cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403			
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser			
90 95 100			
aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451			
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr			
105 110 115			
cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499			



His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu
 120 125 130

tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547
 Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val
 135 140 145

gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595
 Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp
 150 155 160 165

gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643
 Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe
 170 175 180

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691
 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln
 185 190 195

acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739
 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr
 200 205 210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787
 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala
 215 220 225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835
 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro
 230 235 240 245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883
 Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro
 250 255 260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931
 Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile
 265 270 275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979
 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala
 280 285 290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc
 1027
 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile
 295 300 305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt
 1071
 Gly Arg Val Ala Ala Gln Gln
 310 315

<210> 1088
 <211> 316
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1088
 Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

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Leu Ala Leu Ala Tyr Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly	20	25	30
Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln	305	310	315

<210> 1089



<211> 366
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(343)
 <223> RXC00540

<400> 1089
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 Val Ala Arg Val Val
 1 5
 gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163
 Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
 10 15 20
 gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211
 Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
 25 30 35
 cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259
 Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
 40 45 50
 gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307
 Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
 55 60 65
 gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353
 Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
 70 75 80
 aatcggtgtc att 366

<210> 1090
 <211> 81
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1090
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 Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
 20 25 30
 Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
 35 40 45
 Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
 50 55 60
 Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
 65 70 75 80
 Lys



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<210> 1091
<211> 498
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(475)  
<223> RXC00560
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										atg	agg	att	gat	ccg		
										Met	Arg	Ile	Asp	Pro		
										1				5		
ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg															163	
Leu	Glu	Thr	Arg	Gln	Ala	Val	Leu	Ala	Val	Lys	Asp	Trp	Ile	Glu	Gly	
				10					15					20		
gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act															211	
Glu	Gly	Asp	Val	Lys	Lys	Pro	Gly	Arg	Ala	Ala	Leu	Ala	Ala	Ala	Thr	
			25					30				35				
cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg															259	
Arg	Leu	Ser	Val	Arg	Leu	Leu	Ala	Gln	His	Ala	Pro	Gly	Asn	Ser	Val	
		40					45					50				
gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca															307	
Glu	Val	Arg	Val	Pro	Pro	Phe	Val	Ala	Val	Gln	Cys	Ile	Glu	Gly	Pro	
	55					60					65					
aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag															355	
Lys	His	Thr	Arg	Gly	Thr	Pro	Pro	Asn	Val	Val	Glu	Thr	Asp	Ala	Lys	
	70				75					80				85		
acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt															403	
Thr	Trp	Leu	Arg	Leu	Ala	Pro	Gly	Gln	Thr	Thr	Phe	Asp	Ala	Glu	Phe	
				90				95						100		
gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg															451	
Glu	Ser	Gly	Lys	Ile	Ser	Ala	Ser	Gly	Thr	Arg	Ala	Lys	Glu	Ile	Ala	
			105					110					115			
gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt															498	
Asp	Trp			Pro	Val	Val	Lys	Leu								
		120					125									

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<210> 1092
<211> 125
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1092
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  1             5             10             15
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Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
 20 25 30
 Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35 40 45
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
 100 105 110
 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 1093

<211> 1305

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1282)

<223> RXC01088

<400> 1093

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 gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115
 Met Gly Leu Trp Ile
 1 5
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70 75 80 85
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg
1027
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc
1075
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa
 1123
 Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
 330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat
 1171
 Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
 345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca
 1219
 Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
 360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg
 1267
 Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
 375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct
 1305
 Gln Gly Thr Thr Glu
 390

<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu
 1 5 10 15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln
 20 25 30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
 35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
 50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
 65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
 85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
 100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
 115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
 130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
 145 150 155 160



Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
 275 280 285
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
 290 295 300
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
 305 310 315 320
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
 325 330 335
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
 340 345 350
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
 355 360 365
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val
 370 375 380
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
 385 390

<210> 1095

<211> 1419

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1396)

<223> RXC02624

<400> 1095

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ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115

																Val Leu Ile Pro His
																1 5
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg	163
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met	
				10					15					20		
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu	
				25					30					35		
tgg	ctt	tcc	cta	aat	ctc	ggg	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile	
				40					45					50		
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc	307
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala	
				55					60					65		
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu	
				70					75					80		
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala	
				90					95					100		
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu	
				105					110					115		
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc	499
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser	
				120					125					130		
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg	
				135					140					145		
cgc	tac	ggg	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Gln	Ala	Ile	Thr	Gln	Ala	
				150					155					160		
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg	643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val	
				170					175					180		
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggg	tac	691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr	
				185					190					195		
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
				200					205					210		
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro	
				215					220					225		
ctt	tac	ttc	ggg	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val	

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg	425	430		
ctg				
1419				

<210> 1096

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
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Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
 275 280 285



Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala
 290 295 300
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn
 305 310 315 320
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly
 325 330 335
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys
 340 345 350
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu
 355 360 365
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu
 370 375 380
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp
 385 390 395 400
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr
 405 410 415
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
 420 425 430

<210> 1097

<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> RXC02665

<400> 1097

caaggcgacc caatggcggt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

atcaccgacg aagccgaacc cacaatat tt gaggtaccag gtg act aac cca atc 115
 Val Thr Asn Pro Ile
 1 5

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
 10 15 20

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys
 25 30 35

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
 40 45 50



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ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
    55                      60                      65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
    70                      75                      80                      85

ggt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
                      90                      95                      100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
                      105                      110                      115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
                      120                      125                      130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
                      135                      140                      145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
    150                      155                      160

ggc 603

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<210> 1098

<211> 160

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1098

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Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
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Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
                      20                      25                      30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
                      35                      40                      45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
                      50                      55                      60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
                      65                      70                      75                      80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
                      85                      90                      95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
                      100                      105                      110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
                      115                      120                      125

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Pro	Cys	Ser	Leu	Ser	Ala	Thr	Thr	Thr	Asp	His	Met	Gly	Phe	Thr	Gly
130						135					140				
Arg	Ser	Glu	Gly	Arg	Ala	Ser	Val	Ala	Thr	Ala	Val	Val	Trp	Lys	Ala
145					150					155					160

<210> 1099

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

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ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115
                                         Met Leu Val Ala Ala
                                         1                               5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
                               10                               15                               20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
                               25                               30                               35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
                               40                               45                               50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
                               55                               60                               65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
                               70                               75                               80                               85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
                               90                               95                               100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
                               105                               110                               115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
                               120                               125                               130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

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135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg			595
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu			
150	155	160	165
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag			643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu			
	170	175	180
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct			691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro			
	185	190	195
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag			739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu			
	200	205	210
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc			787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe			
	215	220	225
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg			835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala			
	230	235	240
ggt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc			883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala			
	250	255	260
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag			931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu			
	265	270	275
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att			979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile			
	280	285	290
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc			
1027			
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala			
	295	300	305
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt			
1075			
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val			
	310	315	320
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat			
1123			
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp			
	330	335	340
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg			
1171			
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val			
	345	350	355
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat			
1219			
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			



360 365 370
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga
 1267
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
 375 380 385

 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt
 1315
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
 390 395 400 405

 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt
 1363
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
 410 415 420

 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag
 1411
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
 425 430 435

 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat
 1459
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
 440 445 450

 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg
 1507
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
 455 460 465

 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta
 1555
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 1603
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
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 1651
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
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 Ser Arg Ser Glu Glu
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 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
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 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
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 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
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 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
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 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
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 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
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 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
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 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
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 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
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 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
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 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
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 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
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 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
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 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
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 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
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<212> DNA

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<222> (101)..(385)

<223> RXC02238

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 Val Thr Asn Val Ser 5
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 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 20
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 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 35
 25 30



gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
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act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
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cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

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 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
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<220>

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<222> (1)..(1275)

<223> RXC01946

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gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144	
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln		
		35					40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192	
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly		
		50				55					60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240	
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His		
65					70					75					80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288	
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His		
				85					90					95			
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336	
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala		
			100					105					110				
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384	
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp		
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gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432	
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp		
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gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480	
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly		
145					150					155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528	
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala		
				165					170					175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576	
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn		
			180					185					190				
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624	
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro		
		195					200					205					
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672	
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr		
		210				215					220						
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Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile		
225					230					235					240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggc	gca	ggt	aaa	768	
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys		
				245					250					255			
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggt	gtg	gaa	cgc	acc	gac	ggc	gaa	816	
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu		

260	265	270	
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Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln			
275	280	285	
gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc			912
Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile			
290	295	300	
gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga			960
Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly			
305	310	315	320
tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc			
1008			
Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu			
	325	330	335
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cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg			
1104			
Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro			
	355	360	365
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1152			
Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala			
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gtc gtc ctg gtt acc cac gac ccg ggt gca gtc aag gcc ctt gag cca			
1200			
Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro			
	385	390	395
gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat			
1248			
Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp			
	405	410	415
cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat			
1295			
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gct			
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 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
 35 40 45
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
 50 55 60
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
 65 70 75 80
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
 85 90 95
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
 100 105 110
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
 115 120 125
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
 130 135 140
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
 145 150 155 160
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
 165 170 175
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
 180 185 190
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
 195 200 205
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
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 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
 225 230 235 240
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
 245 250 255
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
 260 265 270
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
 275 280 285
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
 290 295 300
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
 305 310 315 320
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala
 420 425

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 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(613)
 <223> RXN03171

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 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
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ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
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<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1106

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 35 40 45
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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<210> 1107



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<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(613)  
<223> FRXA02857
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Met Asp Ile Thr Ile																
1 5																
gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag																163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu																
10 15 20																
cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc																211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala																
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Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp																
40 45 50																
acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca																307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro																
55 60 65																
ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca																355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro																
70 75 80 85																
gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc																403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala																
90 95 100																
cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca																451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro																
105 110 115																
cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc																499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala																
120 125 130																
acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc																547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly																
135 140 145																
gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg																595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val																
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<210> 1108
 <211> 171
 <212> PRT
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<400> 1108

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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
             35             40             45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
             50             55             60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
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Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
             85             90             95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
             100            105            110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
             115            120            125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
             130            135            140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
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Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
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<222> (101)..(424)

<223> RXN00450

<400> 1109

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                               Val Gly Val Leu Pro
                               1             5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
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 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
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att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga cgc atc 424
 Gly Ala Arg Ile Gly Arg Ile
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<210> 1110

<211> 108

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1110

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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
 100 105

<210> 1111

<211> 418

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(418)



<223> FRXA00450

<400> 1111

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga 418
 Gly Ala Arg Ile Gly
 105

<210> 1112

<211> 106

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
 100 105

<210> 1113
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00465

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 Met Thr Glu Asp Asp
 1 5
 tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
 10 15 20
 cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
 25 30 35
 gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
 40 45 50
 cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
 55 60 65
 tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
 70 75 80 85
 atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
 90 95 100
 gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
 105 110 115
 gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
 120 125 130
 ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
 135 140 145
 ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
 150 155 160

tagcgctggg catgtgactt taa

615

<210> 1114

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1114

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Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35					40					45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
50						55					60				

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
			85						90					95	

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
			100					105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
130					135						140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

<210> 1115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXA00717

<400> 1115

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tcaatttcat	acgttttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggt ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile
 250 255 260
 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu
 265 270 275
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val
 280 285 290
 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct
 1027
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser
 295 300 305
 gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg
 1080
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
 310 315 320
 cct
 1083
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 <211> 320
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 <213> *Corynebacterium glutamicum*
 <400> 1116
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 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly
 20 25 30
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile
 35 40 45
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp
 50 55 60
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val
 65 70 75 80
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His
 85 90 95
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile
 100 105 110
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg
 115 120 125
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val
 130 135 140
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln
 165 170 175
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu
 180 185 190
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys
 195 200 205
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr
 210 215 220
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly
 225 230 235 240
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys
 245 250 255
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg
 260 265 270
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr
 275 280 285
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg
 290 295 300
 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
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<210> 1117

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(955)

<223> RXA01894

<400> 1117

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 Met Pro Lys Pro Lys
 1 5

aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
 10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
 25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile 55 60 65			307
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met 70 75 80 85			355
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt Val Ile Ser Ser Tyr Pro Ser 280 285			978



<210> 1118
 <211> 285
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1118

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      20              25              30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
      35              40              45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
  50              55              60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
  65              70              75              80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
      85              90              95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
      100             105             110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
      115             120             125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
      130             135             140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
      145             150             155             160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
      165             170             175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
      180             185             190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
      195             200             205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
      210             215             220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
      225             230             235             240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
      245             250             255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
      260             265             270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(856)
 <223> RXA02536

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 Met Asp Asn Phe Ala
 1 5
 ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
 10 15 20
 ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
 25 30 35
 gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
 40 45 50
 aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
 55 60 65
 cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
 70 75 80 85
 aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
 90 95 100
 att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115
 ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130
 gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145
 gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165
 ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala

170 175 180
 ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
 185 190 195
 gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
 200 205 210
 atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
 215 220 225
 cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
 230 235 240 245
 cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879
 Arg Glu Ala Leu Pro Val Leu
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<210> 1120

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

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 35 40 45
 Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
 50 55 60
 Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr
 65 70 75 80
 Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His
 85 90 95
 Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu
 100 105 110
 Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp
 115 120 125
 Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
 130 135 140
 Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
 145 150 155 160
 Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
 165 170 175



Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
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Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 1121

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 1121

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 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggg ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggg ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	
1027	
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	
1075	
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	
1123	
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly	
330 335 340	

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
455 460 465

gcc gcc ggc gaa agc gtg gaa
1528

Ala Ala Gly Glu Ser Val Glu
470 475

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

 <210> 1123
 <211> 1528
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1528)
 <223> FRXA01209

 <400> 1123
 cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggtt tattgatgcg 60

 ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

 gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

 tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

 gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

 cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

 ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag gcc atc gct gag 595
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggc gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528

Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 1124

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
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Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355	360	365
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn		
370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
	450	455
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475
<210> 1125		
<211> 795		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(772)		
<223> RXN01617		
<400> 1125		
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tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115		
		Leu Ile Leu Lys Thr 5
act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163		
		Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn 20
cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211		
		Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile 35
ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259		
		Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu 50
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307		
		Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys 65
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355		
		Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg 85



gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu
 90 95 100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu
 105 110 115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val
 120 125 130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
 135 140 145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp
 150 155 160 165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala
 170 175 180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
 185 190 195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro
 200 205 210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc 792
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 215 220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
 1 5 10 15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr



85								90				95			
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu
			100					105					110		
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly
		115					120					125			
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn
	130					135					140				
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu
145					150					155					160
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala
				165					170					175	
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala
			180					185					190		
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val
		195					200					205			
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys
	210					215					220				

<210> 1127

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (615)

<223> FRXA01617

<400> 1127

gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1				5				10						15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
		35					40					45				
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
	50					55					60					
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65				70						75				80		

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp 95
 85 90 95

 gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr 110
 100 105 110

 gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp 125
 115 120 125

 gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile 140
 130 135 140

 ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile 160
 145 150 155 160

 acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr 175
 165 170 175

 gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn 190
 180 185 190

 gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys 205
 195 200 205

 aaacaagctc cct 638

<210> 1128

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15

 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

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tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tgc aag atg 115
 Met Val Ser Lys Met
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
 25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
 105 110 115
 att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
 120 125 130
 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
 135 140 145
 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
 150 155 160 165
 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
 170 175 180
 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
 185 190 195
 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
 200 205 210
 cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220
 aaa 792

<210> 1130

<211> 223

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
 1 5 10 15
 Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
 20 25 30
 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45
 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60
 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80
 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95
 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110



Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
210 215 220

<210> 1131

<211> 726

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> RXC01622

<400> 1131

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gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
Met Ser Asp Phe Tyr
1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
 135 140 145
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
 150 155 160 165
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
 170 175 180
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726
 Pro Ser Asp Asn
 200

<210> 1132

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
 1 5 10 15
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
 Val Ser Lys Ile Ser
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	
1027	
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg	
1075	
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	
1123	
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
 1171
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
 1219
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
 1267
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
 1411
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
 1459
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
 1507
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
 1555
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
 1603
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
 1651
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530



gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205



Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro



1545



gat

555

<210> 1136

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
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Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 130 135 140

<210> 1137

<211> 898

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXC02207

<400> 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
 Met Arg Arg Arg Ser
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
 10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
25 30 35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
150 155 160 165	
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
170 175 180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
200 205 210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
215 220 225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
250 255 260	

cac cga cga gga acc
His Arg Arg Gly Thr
265

898

<210> 1138

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
260 265



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<210> 1139
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(868)
<223> RXA00347
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<400> 1139																
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aaagtgccag	gggttctgtg	ggatccgtac	actgggtccc	atg	act	ttg	act	att	115							
				Met	Thr	Leu	Thr	Ile								
				1				5								
gag	gaa	atc	gcc	aag	acc	aaa	aag	ctt	ttg	ggt	gtg	tcc	gat	ttt	gat	163
Glu	Glu	Ile	Ala	Lys	Thr	Lys	Lys	Leu	Leu	Val	Val	Ser	Asp	Phe	Asp	
				10					15					20		
gga	acc	atc	gca	gga	ttt	agc	aag	gac	gct	tac	aac	ggt	cct	atc	aac	211
Gly	Thr	Ile	Ala	Gly	Phe	Ser	Lys	Asp	Ala	Tyr	Asn	Val	Pro	Ile	Asn	
			25					30					35			
cag	aaa	tcc	ctc	aag	gcg	gta	aaa	gac	ctc	tcc	caa	caa	gca	gac	act	259
Gln	Lys	Ser	Leu	Lys	Ala	Val	Lys	Asp	Leu	Ser	Gln	Gln	Ala	Asp	Thr	
		40					45					50				
gat	ggt	gtc	att	ttg	tcg	gga	cgt	cac	ctg	gag	gga	ttg	aag	acg	ggt	307
Asp	Val	Val	Ile	Leu	Ser	Gly	Arg	His	Leu	Glu	Gly	Leu	Lys	Thr	Val	
	55					60					65					
ctt	gat	ctt	ggt	cag	tac	gac	atc	acc	atg	gtg	ggt	tca	cac	ggt	tct	355
Leu	Asp	Leu	Gly	Gln	Tyr	Asp	Ile	Thr	Met	Val	Gly	Ser	His	Gly	Ser	
70					75					80					85	
gag	gat	tcc	tcc	cgc	ccg	cgt	acc	ctc	act	cct	gaa	gag	gta	gct	cgc	403
Glu	Asp	Ser	Ser	Arg	Pro	Arg	Thr	Leu	Thr	Pro	Glu	Glu	Val	Ala	Arg	
				90					95					100		
ctc	gcc	aag	att	gaa	gca	gat	ctg	gaa	aag	atc	gtc	gac	ggc	atc	gaa	451
Leu	Ala	Lys	Ile	Glu	Ala	Asp	Leu	Glu	Lys	Ile	Val	Asp	Gly	Ile	Glu	
			105					110					115			
ggc	gca	ttc	gtg	gag	atc	aag	cct	ttc	cac	cgc	gtg	ctg	cac	ttc	atc	499
Gly	Ala	Phe	Val	Glu	Ile	Lys	Pro	Phe	His	Arg	Val	Leu	His	Phe	Ile	
		120					125					130				
cgt	ggt	tcc	gac	aag	gac	aaa	gtc	caa	gga	atc	ctc	gcc	caa	gca	gca	547
Arg	Val	Ser	Asp	Lys	Asp	Lys	Val	Gln	Gly	Ile	Leu	Ala	Gln	Ala	Ala	
	135					140					145					
cac	gta	gac	tct	tcc	ggc	ctg	aag	ggt	act	aac	ggc	aag	agc	atc	atc	595
His	Val	Asp	Ser	Ser	Gly	Leu	Lys	Val	Thr	Asn	Gly	Lys	Ser	Ile	Ile	
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Glu	Tyr	Ser	Ile	Ser	Ser	Thr	Thr	Lys	Gly	Thr	Trp	Leu	Lys	Glu	Tyr	

	170	175	180	
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Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr				
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acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta				739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu				
	200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac				787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp				
	215	220	225	
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc				835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg				
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<213> Corynebacterium glutamicum

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Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser			
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Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu			
50 55 60			
Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val			
65 70 75 80			
Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro			
85 90 95			
Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile			
100 105 110			
Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg			
115 120 125			
Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile			
130 135 140			
Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn			
145 150 155 160			

Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr
 165 170 175
 Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe
 180 185 190
 Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn
 195 200 205
 Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala
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 Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys
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 <223> RXN01239

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 Met Ala Arg Pro Ile
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 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
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 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu
 25 30 35
 aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
 40 45 50
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 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
 55 60 65
 aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
 70 75 80 85
 aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His

90										95					100					
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta	451																			
Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu																				
105 110 115																				
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg	499																			
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp																				
120 125 130																				
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt	547																			
His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly																				
135 140 145																				
gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag	595																			
Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu																				
150 155 160 165																				
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc	643																			
Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr																				
170 175 180																				
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg	691																			
Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu																				
185 190 195																				
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg	739																			
Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val																				
200 205 210																				
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat	787																			
Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His																				
215 220 225																				
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc	835																			
Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly																				
230 235 240 245																				
gtg cgc gtc gat cac ccc gac ggc ctt tcc gat cct ttt gga tat ctg	883																			
Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu																				
250 255 260																				
cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa	931																			
His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu																				
265 270 275																				
aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat	979																			
Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp																				
280 285 290																				
ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc																				
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1075																				
Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser																				
310 315 320 325																				



gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc
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 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu
 330 335 340

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 1171
 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu
 345 350 355

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 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
 360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg
 1267
 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
 375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
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 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
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 1363
 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
 410 415 420

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 Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
 425 430 435

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 1459
 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
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 1555
 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
 470 475 480 485

gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
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 Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
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cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg
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 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
 505 510 515



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 1699
 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
 520 525 530

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 1747
 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
 535 540 545

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 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
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 1891
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
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 1939
 Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
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 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln
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 2083
 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg
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 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr
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 Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
 680 685 690

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 2227
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
 695 700 705



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730 735 740

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2371
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745 750 755

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760 765 770

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Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
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Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Ile	Ala	Pro	Gly	Thr	Glu	Glu	Gly	Thr	Pro	Gln	Glu	Val	Tyr	Lys	Arg	
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225					230					235					240	
Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Asp	His	Pro	Asp	Gly	Leu	Ser	Asp	
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Arg	Thr	Thr	Ala	Thr	Val	Ile	Ala	Glu	Met	Ser	Lys	Arg	Phe	Pro	Ser	
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 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
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 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
 485 490 495
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
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 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
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 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
 545 550 555 560
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
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 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
 580 585 590
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
 610 615 620
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
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 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
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 675 680 685
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 690 695 700
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
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<223> FRXA01239

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 40 45 50

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 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
 70 75 80 85

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 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
 90 95 100

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 105 110 115

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 Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp
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gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu 150 155 160 165	595
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr 170 175 180	643
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu 185 190 195	691
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val 200 205 210	739
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His 215 220 225	787
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly 230 235 240 245	835
gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu 250 255 260	883
cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu 265 270 275	931
aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp 280 285 290	979
ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc 1027 Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile 295 300 305	
tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt 1075 Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser 310 315 320 325	
gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc 1123 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu 330 335 340	
aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc 1171 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu 345 350 355	



gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc
1219
Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg
1267
Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
1315
Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
390 395 400 405

gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc
1363
Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
410 415 420

gac ctc atc gcg gcc gcc cta ctt ggc aat ggc gag gcc aaa atc cgc
1411
Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
425 430 435

ttc gct caa gtc tgc ggc gcc gtc atg gct aaa ggt gtg gaa gac acc
1459
Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr
440 445 450

acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc
1507
Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
455 460 465

gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag
1555
Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
470 475 480 485

gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
1603
Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg
1651
His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg
1699
Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac
1747
Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
535 540 545



ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc
 1795
 Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg
 550 555 560 565

gat cga ttc agg gaa tac gcc cta aaa gct atc cgc gaa gca tcc aca
 1843
 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
 570 575 580

aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc
 1891
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
 585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc
 1939
 Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
 600 605 610

gaa ttt gtc tcc cac atc aac cgt ggc tct gtg caa atc tcc tta ggc
 1987
 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
 615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa
 2035
 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln
 630 635 640 645

gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc
 2083
 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg
 650 655 660

ttt gtt gat tac acc gcc aga gaa caa gtc ctg gag cgc ctg caa acc
 2131
 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr
 665 670 675

tgg gat tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc
 2179
 Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
 680 685 690

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct
 2227
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
 695 700 705

gaa ttt cgt gca agc ttt gtt ggt gga gat cat cag gca gta ttt ggc
 2275
 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
 710 715 720 725

gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac
 2323
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
 730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt
2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc
2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
790 795 800 805

gta ccc gat agt gag ttt tgatccctgc acaggaaagt tag
2556

Val Pro Asp Ser Glu Phe
810

<210> 1144

<211> 811

<212> PRT

<213> Corynebacterium glutamicum

<400> 1144

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20 25 30

Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
145 150 155 160



Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
 165 170 175
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
 180 185 190
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
 195 200 205
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro
 210 215 220
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu
 225 230 235 240
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
 245 250 255
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
 260 265 270
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
 275 280 285
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu
 290 295 300
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu
 305 310 315 320
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser
 325 330 335
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala
 340 345 350
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr
 355 360 365
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
 370 375 380
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser
 385 390 395 400
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
 405 410 415
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly
 420 425 430
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys
 435 440 445
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
 450 455 460
 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
 465 470 475 480



Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
 485 490 495
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
 500 505 510
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
 515 520 525
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser
 530 535 540
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
 545 550 555 560
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
 565 570 575
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
 580 585 590
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
 610 615 620
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
 625 630 635 640
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
 645 650 655
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
 660 665 670
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp
 675 680 685
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
 690 695 700
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His
 705 710 715 720
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
 725 730 735
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
 740 745 750
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
 755 760 765
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
 770 775 780
 Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val
 785 790 795 800
 Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe



805

810

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<211> 1953
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(1930)  
<223> RXA02645
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tgatataggt cagaaatcgc gagcgcttga tctctagttc																115
Met Leu Lys Asp Leu																15
acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca																163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser																20
cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg																211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met																35
ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta																259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val																40
cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc																307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly																55
agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt																355
Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly																70
ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc																403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro																90
cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc																451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser																105
gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc																499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu																120
cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat																547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp																135
gga acg ttt gag gga gtc gtc gac aag ctt cct tat ctg cgc gac ctc																595
Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu																150
ggc gtg acc gcc atc gaa ctt tta ccc gtg cag ccc ttt ggc ggc aac																643

Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn	
170	175 180
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc	691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	
185	190 195
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag	739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	
200	205 210
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc	787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	
215	220 225
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc	835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	
230	235 240 245
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa	883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	
250	255 260
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt	931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	
265	270 275
cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc	979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	
280	285 290
ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc	
1027	
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	
295	300 305
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc	
1075	
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	
310	315 320 325
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg	
1123	
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	
330	335 340
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt	
1171	
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	
345	350 355
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca	
1219	
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	
360	365 370
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc	
1267	
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	
375	380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg
1940

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600 605 610

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1953

<210> 1146

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

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20 25 30

Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr
210 215 220



acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc
 1315
 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr
 390 395 400 405

cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc
 1363
 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly
 410 415 420

aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag
 1411
 Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln
 425 430 435

cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg
 1459
 Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met
 440 445 450

ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt
 1507
 Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe
 455 460 465

tgc tcc cac acc gac ccc gag ctc aac cgg cta acc tcc gag ggc cgc
 1555
 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg
 470 475 480 485

aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc
 1603
 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser
 490 495 500

ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc
 1651
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe
 505 510 515

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 1699
 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His
 520 525 530

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 1747
 Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu
 535 540 545

gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga
 1795
 Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg
 550 555 560 565

att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc
 1843
 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly
 570 575 580



Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr
 225 230 235 240
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly
 245 250 255
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln
 260 265 270
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
 275 280 285
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met
 290 295 300
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile
 305 310 315 320
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala
 325 330 335
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala
 340 345 350
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe
 355 360 365
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His
 370 375 380
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val
 385 390 395 400
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr
 405 410 415
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr
 420 425 430
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser
 435 440 445
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr
 450 455 460
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu
 465 470 475 480
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala
 485 490 495
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys
 500 505 510
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr
 515 520 525
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn
 530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala
 545 550 555 560
 Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr
 565 570 575
 Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val
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 Arg Asn
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<211> 832

<212> DNA

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<221> CDS

<222> (101)..(832)

<223> RXN02355

<400> 1147

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 Met Ser Ser Ile Ser
 1 5
 cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163
 Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile
 10 15 20
 gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211
 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser
 25 30 35
 acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met
 40 45 50
 ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn
 55 60 65
 gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355
 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu
 70 75 80 85
 gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403
 Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn
 90 95 100
 tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451
 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe
 105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp
 120 125 130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly
 135 140 145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg
 150 155 160 165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val
 170 175 180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr
 185 190 195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile
 200 205 210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg
 215 220 225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly
 230 235 240

<210> 1148

<211> 244

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1148

Met Ser Ser Ile Ser Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr
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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser
 20 25 30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro
 35 40 45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile
 50 55 60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn
 65 70 75 80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser
 85 90 95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile
 100 105 110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
145	150	155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
210	215	220
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala		
225	230	235
240		
Leu Val Asp Gly		

<210> 1149
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXN02909

<400> 1149
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 atagtttcct ggattgtttg gcacagtcgg gagaaaactc atg aac cgc gca cga 115
 Met Asn Arg Ala Arg
 1 5
 atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163
 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys
 10 15 20
 ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211
 Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn
 25 30 35
 att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259
 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
 40 45 50
 tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307
 Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr
 55 60 65
 ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355



Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu
 70 75 80 85
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp
 90 95 100
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His
 105 110 115
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr
 120 125 130
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547
 Ser Gly Ser Glu Ile Leu Thr Ser Asp Val Asp Glu Leu Asp Arg
 135 140 145
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcca 596
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser
 150 155 160
 gggctttaaa gtg 609

<210> 1150

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1150

Met Asn Arg Ala Arg Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu
 1 5 10 15
 Leu Leu Ala Ser Cys Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr
 20 25 30
 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile
 35 40 45
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser
 50 55 60
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe
 65 70 75 80
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr
 85 90 95
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln
 100 105 110
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe
 115 120 125
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val
 130 135 140
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro
 145 150 155 160

Thr Ser

<210> 1151

<211> 1590

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1567)

<223> RXS00349

<400> 1151

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gtgattggac	tcttttttct	tgcaaaatgt	tttccagcgg	atg	ttg	agt	ttt	gcg	115
				Met	Leu	Ser	Phe	Ala	
				1				5	

acc	ctt	cgt	ggc	cgc	att	tca	aca	ggt	gac	gct	gca	aaa	gcc	gca	cct	163
Thr	Leu	Arg	Gly	Arg	Ile	Ser	Thr	Val	Asp	Ala	Ala	Lys	Ala	Ala	Pro	
				10					15					20		

ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val	
			25					30					35			

gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	
		40				45						50				

tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	gtt	cga	gca	gtg	acc	307
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	
	55					60					65					

tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	
70					75					80				85		

atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	
				90					95					100		

gtg	ttt	cat	gtt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	
			105					110					115			

gag	gtt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	
			120				125					130				

gag	gtt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	
		135				140					145					

tat	ggt	ttc	cct	gtt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	
150					155				160						165	



ggt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt	643
Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe	
170 175 180	
att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag	691
Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys	
185 190 195	
ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg	739
Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr	
200 205 210	
ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag	787
Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu	
215 220 225	
atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca	835
Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala	
230 235 240 245	
ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg	883
Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro	
250 255 260	
gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc	931
Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly	
265 270 275	
att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat	979
Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His	
280 285 290	
gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct	
1027	
Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser	
295 300 305	
aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca	
1075	
Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala	
310 315 320 325	
gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act	
1123	
Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr	
330 335 340	
gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc	
1171	
Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly	
345 350 355	
ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt	
1219	
Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly	
360 365 370	
ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att	
1267	
Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile	

375 380 385
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg
 1315
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met
 390 395 400 405
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg
 1363
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala
 410 415 420
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt
 1411
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly
 425 430 435
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac
 1459
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr
 440 445 450
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag
 1507
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu
 455 460 465
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc
 1555
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe
 470 475 480 485
 ggt aat aaa agg taaaaatcaa cctgcttagg cgt
 1590
 Gly Asn Lys Arg

<210> 1152
 <211> 489
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1152
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 Ala Lys Ala Ala Pro Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr
 20 25 30
 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly
 35 40 45
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
 50 55 60
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
 65 70 75 80
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
 85 90 95



Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
 100 105 110
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
 115 120 125
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
 130 135 140
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
 145 150 155 160
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
 165 170 175
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
 180 185 190
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
 195 200 205
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
 210 215 220
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
 225 230 235 240
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
 245 250 255
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
 260 265 270
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
 275 280 285
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
 290 295 300
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
 305 310 315 320
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
 325 330 335
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
 340 345 350
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
 355 360 365
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
 370 375 380
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
 385 390 395 400
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
 420 425 430
 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
 435 440 445
 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
 450 455 460
 Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
 465 470 475 480
 Thr Asn Gln Arg Phe Gly Asn Lys Arg
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<210> 1153

<211> 440

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(417)

<223> RXS03183

<400> 1153

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 Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly
 1 5 10 15
 aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
 20 25 30
 aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45
 atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
 50 55 60
 cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80
 cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
 85 90 95
 cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110
 gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125
 gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser



130 135 440
ttc

<210> 1154
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 1154
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Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
20 25 30
Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
35 40 45
Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
50 55 60
Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
65 70 75 80
Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
85 90 95
Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
100 105 110
Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
115 120 125
Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser
130 135

<210> 1155
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXC00874

<400> 1155
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tctgggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa 115
Met Ser Ile Gly Gln
1 5
cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163
His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
10 15 20
aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala	
25 30 35	
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat	259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
40 45 50	
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
55 60 65	
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca	355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
70 75 80 85	
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
90 95 100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
105 110 115	
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
120 125 130	
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc	835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	

265 270 275
 cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
 280 285 290
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac
 1027
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
 295 300 305
 gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa
 1075
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
 310 315 320 325
 gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc
 1123
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
 330 335 340
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg
 1171
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
 345 350 355
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 1212
 Val Glu Arg Leu Leu Asp
 360
 <210> 1156
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 <213> Corynebacterium glutamicum
 <400> 1156
 Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys
 1 5 10 15
 Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly
 20 25 30
 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
 35 40 45
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
 50 55 60
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
 65 70 75 80
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
 85 90 95
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
 100 105 110
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
130 135 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
145 150 155 160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
165 170 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
180 185 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
195 200 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
210 215 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
225 230 235 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
245 250 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
260 265 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
275 280 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
290 295 300

Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
305 310 315 320

Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
325 330 335

Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
340 345 350

Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
355 360